## STIC-Biotech/ChemLib

From: Sent: To:

Subject:

Davis, Minh-Tam
Tuesday, November 05, 2002 4:18 PM
STIC-Biotech/ChemLib
Search request for 09/899569

SEQ ID NO: 3 and 4 Thank you. MINH TAM DAVIS ART UNIT 1642, ROOM 8A01, MB 8E12 305-2008

Mary Jane Ruhl Tech. Info. Specialist, STIC TC-1600 CM-1, Room 6A-06 Phone: 605-1155

Searcher:	
Phone:	
Location:	
Date Picked Up:	
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Searcher Prep/Review:	
Clerical:	
Online time:	

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (where	applic.)
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DIALOG:	
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DRLink:	
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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12325.991 Million cell updates/sec
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AAS63196
AAA26351
AAS21324
ABV30293
AAA108379
AAA78075
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Human immune/haema	AAK77836	22	44354	3.6	224.6	ŭ
Human immune/haema	AAK77833	22	44354	3.6	224.6	4
Human nervous syst	ABA21323	22	2816	3.7	225.4	ũ
Human cDNA sequenc	AAH17880	22	2512	3.7	225.4	Ñ
Human reproductive	AAL06210	22	626	3.7	225.4	ب
Human osteoblast d	ABQ88139	24	103747	3.7	225.6	Ö
DNA encoding novel	AAS27780	22	11336	3.7	225.6	9
Human Claspin geno	ABK52612	24	58837	3.7	226	<u>~</u>
Human immune/haema	AAK73225	22	9359	3.7	226	7
cDNA encoding huma	ABK51416	24	3121	3.7	226	5
Human DNA repair a	AAS32232	22	32195	3.7	226.2	G
	AAI97423	22	806	3.7	226.4	4
Human reproductive	AAL04404	22	14769	3.7	226.6	ũ
	AAH16255	22	3173	3.7	227	<sub>ເ</sub>
	ABL45808	24	9163	3.7	227.2	Ï
mmune/ha	AAK87078	22	305	3.7	230.2	ō
cancer	ABL67239	24	167343	. 3.7	230.8	ĕ
a	ABL64403	24	167343		w	8
Human musculoskele	AAL36242	22	5199		231	7
	AAL36240	22	5157	•	231	ð
	ABL97825	23	32249		231.4	ŭ
-	AAL04931	22	32249		231.4	4
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ovarian	ABL86888	24	339		339	ï
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	AAS23308	22	400		380.4	œ
	AAH98628	22	478	•	427.4	7
cDNA #393 encoding	AAS57717	23	535		482	Ō
. DNA encoding novel	AAS64483	23	487	•	482	'n
Human colon cancer	AAZ80286	21	636	•	489.2	4
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## ALIGNMENTS

## Human tumour-associated antigen B345 cDNA SEQ ID NO 17-MAY-2002 ABA99507; ABA99507 standard; cDNA; 6163 BP. (first entry)

Tumour-associated antigen; human; B345; cytostatic; cell communication; cell interaction; signal transduction; metastasis; cancer; colon; immunotherapy; carcinoma; lung; diagnosis; gene; ss.

Homo sapiens

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RESULT 1
ABA99507
ID ABA99
XX ABA9
AC ABA9
AC ABA9
AX Tuma
XX Tuma
KW Celll
KW Immu
OS HOMC
XX HOMC
EFT 5'U7
FT GC_s
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Best Local Similarity
Matches 6163; Conser
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P-PSDB;
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70	AGTTGGCCACTGAGGAGCCACCTCCTCGCTCCCCTCCTGAGTCTGAGAGTGAACCGTAC	2641	В
	TTGGCCACTGAGGAGCCACCTCCTCGCTCCCCTCCTGAGTCTGAGAGTGAACCGT	64	οy
	GGCACCATGGGGGTCTGTCCTCCCTCCCCACCCATATGCTCCAGGGCCCCAACTGCA	G	밁
2640	GCACCATGGGGGTCTGTCCTCCCCCCCCCCCCACCATATGCTCCAGGGCCCCAACTGC	2581	Ş
2580	CTACAGGATTCCAGCGGCTCCTTCCTGCAGCCAGAGGTGGACACCTACCGGCCGTTCCAG	2521	8
2580	TACAGGATTCCAGCGGCTCCTTCCTGCAGCCAGAGGTGGACACCTACCGGCCGTTCC	2521	δ
2520	AAGGACAATGACTCCCATGTGTATGCAGTCATCGAGGACACCATGGTATATGGGCATCTG	2461	밁
2520	GACAATGACTCCCATGTGTATGCAGTCATCGAGGACACCATGGTATATGGGCATC	2461	Ş
2460	TACAATGGCAACATCAATACTGAGATGCCGAGGCAGCCAAAAAAGTTTCAGAAAAGGCGGA	2401	В
2460	ACAATGGCAACATCAATACTGAGATGCCGAGGCAGCCAAAAAAGTTTCAGAAAGGGCG	2401	Ş
2400	ATCATTTGCTGTGAAAAAGAAGAAGAAAAAAGAAGGGCCCCGCTGTGGGTATC	2341	밁
2400	TTGCTGTGTGAAAAAAGAAGAAAAAGAAGACAAACAAGGGCCCCGCTGTGGGT	-	Ş
2340		2281	밁
2340	ACTGTCATCCTCATCGCAGCGGTGGGAGCTGGAGTCTTACTGCTGTCTGCCCTCGGGCT	œ	õ
2280	AGCGGCAAGCAGCTAGACCTGCTCTTCTCGGTGACACTTACCCCAAGGACTGTGGACTTG	. 2221	밁
	CGGCAAGCAGCTAGACCTGCTCTTCTCGGTGACACTTACCCCAAGGACTGTGG	2221	δ
2220	CATCACAGCTTCTGGGTCAACATC	2161	В
2220	CCAAGCCAAGCTTCCACCATCACAGCTTCTGGGTCAACATCTCTAACTGCAGCCCCA	2161	Ş
2160	ATCATCCAGGAGCAGCAGCCCGGGCTGAGGAGATCTTCAGCCTGGACGAGGATGTGCTC	2101	망
2160	ATCCAGGAGCAGCGGACCCGGGCTGAGGAGATCTTCAGCCTGGACGAGGATGTGC	2101	Qγ
2100		2041	₽ ·
2100	GCCTGACTTTCTTTAAGGAGCGGAGCGGCGTGGTCTGCCAGACAGGGCGCGCATTCAT	2041	δ
2040	TGTGT	1981	밁
2040	GCCTGCCATCCCTCACCTCTGTGTCCTGGAACATCAGCGTGCCCAGAGACCAGGTGGC	1981	γ
1980	ACC	1921	밁
1980	TCACGGTGACCCCTGACACAAAAAGCAAGGTCTACCTGAGGACCCCCAACTGGGACCG	1921	γQ
92		1861	밁
1920	AGGCCTCCAGGCAGGGTCTGACGGTGTCCTTTATACCTTATTTCAAAGAGGAAGGCGTT	1861	δ
1860	ACCTTTGCCCCCAGCTTCCAACAA	1801	뭥
1860	CAGGTGAAGCAGAACATCTCGGTGACCCTTCGCACCTTTGCCCCCAGCTTCCAAC	1801	Qy
1800	GCCATACCCAGCCAGGACCTGTACTTCGGCTCCTTCTGCCCGGGAGGCTCTATCAAGCAG	1741	밁
1800	ATACCCAGCCAGGACCTGTACTTCGGCTCCTTCTGCCCGGGAGGCTCTATCAAGC	1741	Ş
1740	CTGCAGCATACACACGAGAAGCCCTGCAACACCAGCTTCAGCTACCTCGTGGCCAGT	1681	В
1740	CAGCAGCATACACACGAGAAGCCCTGCAACACCAGCTTCAGCTACCTCGTGGCCAG	1681	ρ
1680	TCCTGGAAGCTGCTGGTGCCCAAGGACAGGCTCAGCCTGGTGCTGGTGCCAGCCCAGAAG	1621	В
1680	TGGAAGCTGCTGGTGCCCAAGGACAGGCTCAGCCTGGTGCTGGTGCCAGCCCAG	1621	ρ

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Фу 378	Db 372	Оу 372	Db 366	Qу 366	Db 360	Оу 360	Db 354	Qу 354	Db 348	Оу 348	Db 342	Оу 342	Db 336	Оу 336	Db 330	0у 330	Db 324	Оу 324	Db 318	Qу 318	Db 312	Оу 312	Db 306	0у 306	Db 300	0у 300	_	Оу 294	Db 288	Оу 288	Db 282	Оу 282	Db 276	Qy 276	Db 270	Qy 2701
1 GAATGAAAATCAAGGTGTCAGCAGAGCTGTGCTCCTTCTGAAGGCTCTAGGGAGAAGCCG 3	1 CTTAAAAACAACACATTAGCTTATAGTCCTGGGGATCAGAATTCCAAAATGGATGTCCCT 3	TAAAAACAACACATTAGCTTATAGTCCTGGGGATCAGAATTCCAAAATGGATC	GCCCCCTGCATTAGTTTCTGTTGCCACTGCAACCCATTACT	CAAACAGTGGCCCCCTGCATTAGTTTTCTGTTGCCACTGCAACCCCATTACTTGGTAG 3	ragagaatattctcatcctctaaaaatgtttaaatat	TTTAAAGAGAAATTTAGAGAATATTCTCATCCTCTAAAAATGTTTAAATATA 3	GTTCTCCTAGCTGCAGCAATA 3	TAGCAATAAGAGAAATTTCCTCAAGTTTCCATGTGCGGTTCTCCTAGCTGCAGCAATA 3	1 TAGGTCGGTTCGTGGTTATCCCATTGTGGAAATTCATCTTGAATCCCATTGTCCTATAGT 3	GGTTCGTGGTTATCCCATTGTGGAAATTCATCTTGAATCCCATTGTCCTATAGT 3	1 ATGTGTGTGTTTGAGCAGCATTGACACATATCTGCTTTGATAAGAGACTTCCTGATTCTC 3	TTTGAGCAGCATTGACACATATCTGCTTTGATAAGAGACTTCCTGATTCTC 3	AAACGTGTGCCTGTCCCCCAGGTGGTGGGAATAATTTACAATCTGTCCAACCAGAAAAAA 3	стетсссссае в поставляющий в поставлений в поставляющий в поставля	1 GTAATAACTCATACTGGTTTGGATGCCTGGGTTGTGACTTCTACTGACCGCTAGAT 3	AATAACTCATACTAACTGGTTTGGATGCCTGGGTTGTGACTTCTACTGACCGCTAGAT 3	CACCTGACTTA 3	CTGTGTTATTTAAGAGATCAAATGTATAACCACCTAGCTCTTTTCACCTGACTTA 3	1 CTCTCACTGGGGTCCCCAGGATGAAAACGACAATGTGCCTTTTTATTATTATTTAT	ICACTGGGGTCCCCAGGATGAAAACGACAATGTGCCTTTTTATTATTATTTAT	1 AGAGGCTTGCCCTCTTCAGGACAACAGTTCCCAATTCCAAGGAGCCTACCTGAGGTCCCTA 3	TTGCCCTCTTCAGGACAACAGTTCCAATTCCAAGGAGCCCTACCTGAGGTCCCTA 3	AGAGAGGCCTGAGTCACCTAGCATAGGGTTGCAGCAAGCCCTGGATTCAGAGTGTTAAAC 3	GAGTCACCTAGCATAGGGTTGCAGCAAGCCCCTGGATTCAGAGTGTTAAAC 3		CATGTGCTCCTCAACTTAGGCTGTGCGGTTAGCCAGCCTGTAATGAGAGG 3	1 TCAGTGGACTCATTCTAAGGGCAAGACATTGAAAATGATGAATTCCAATCTGGATACAGT 3	GACTCATTCTAAGGGCAAGACATTGAAAATGATGAATTCCAATCTGGATACAGT 3	1 GAGGAATTATACAGAAGGAACAGCAGGAGGTTTTCCTGGACACCGCCAACTTCACATTGC 2	AGGAATTATACAGAAGGAACAGCAGGAGGTTTTCCTGGACACCGCCAACTTCACATTGC 2	1 GTTTCATAAAGCAGGGCACTGAGACACCCGTCCGTGCTTCCTAAACCAGAAATCCTAAAGAA 2	CATAAAGCAGGGCACTGAGACACCCGTCCGTGTTCCTAACCAGAAATCCTAAAGAA 2		CAGGAGCCCATGGAGCCAGCAGAATAACTTGATCCATTCCAGACGCTTTGCTGA 2		ACCTTCTCCCATCCCAACAATGGGGATGTAAGCAGCAAGGACACAGACATTCCCTTACTG 2
840	780	780	720	720	660	660	600	600	540	540	480	480	420	420	360	360	300	300	240	240	180	180	120	120	060	060	000	000	940	940	088	880	820	820	760	760

	CCTGCTCTGATCTGGAAGGAGAGGGATTATGTTATAGCTTGTCAGCACAGTCCCAAGTT 4920	4861 CC	Qy
	CCCACACCCTCATTTATACCAATTACCTGCCCAGTAACTGTGGACTTTTGCTTCAC 4860	4801 C 4801 C	gb Qy
-·· -	TCCTCCTGCCTCGGCCTCCCAAAGTGCTGGGATTACAGATGTGAGCCACCGCATCCAG 4800	4741 AAT     4741 AAT	р <sub>9</sub>
· ·	TGTAGAGACAGGGTTTCACCATGTTGCCCAGGCTGGTCTCAACCTCCTGGGCTCAAGC 4740	4681 TTT 4681 TTT	B 8
	CCTCCCAAATAGCTGGGATCACTGGCACAAACCACCATGCCCAGCTAATTTTGTATTT 4680	4621 AG    4621 AG	B 8
. • <del>-</del>	GCGCAATCTCGGCTCACTGCAACCTCTGCCTCCTGGGCTCAAGCAATTCTCCCACCTC 4620	4561 TG    4561 TG	Db Qy
· - <del>-</del>	PTTTCTTTTTTTTTAATGTGAGACAGGATCTCAFTCTGTTGCCTAGGCTGGAGTGCAG 4560	4501 T 4501 T	р <i>8</i>
	GAGTAGACCATGAGACCAATGTGTGCTCACATTACCCTTTTTCTTTTTTTT	4441 T 4441 T	p Q
	CCTGCAGGTTGCATTTATTGTAATGAAAAAGAAAGACTGGGATTAATCTCTAATCAGG 4440 	4381 CC 4381 CC	g Qy
-	ACACTACGCCTATCACTTCCCACAATGAGGCTAAGTGTTTGTT	4321 CC 11 4321 CC	р <sub>6</sub>
	GAGCTGGGCACCAGCTCTGCCTTTAGAAGGGGTGTCCACTTCACCAGGTCACCACAGC 4320 	4261 TG    4261 TG	B 8
	CCCAGATCAGAAGATCTGGCCATGCTGGGGCTCACATTCTCACCTAGCAACAACTGGC 4260 	4201 AC 	Оу
	AAAATGATCTGGCGCACAGGGATGTTTTGTTTAGCTTGCGGACTCTAACACTTAAAAA 4200 	4141 C	pb Qy
	GGGGTGCTGTTATTCTGCCTACCACACCTTCCTGCCACTGACTCCCACAGGAGAGGCTA 4140	4081 T 4081 T	рb
	AGCCTTTTGCCATGCAAGACATAGCCACAGGTGGGGATTAGGACCAGGACATCTT 4080	4021 AG    4021 AG	рь
	AAAGCCCACCAGGAAGATCCAGGATAATCTCTCCATCTAAAGATCCTTCATCATCCTGGA 4020 	3961 AA 3961 AA	D Q
	GCTTTTCTCACATGGCATCACTGTGACACTGGCCCTCCCACTTCCCTCTTTGACTTAC 3960 	3901 AAG     3901 AAG	рь
	FTCCTTGCCATTICAAGCTTCTAGAGGCTGGCTGCATTCCCAGGCTCCAGTGGCTGGTC 3900	3841 G 3841 G	g &
		3781 GAA	밁

6000	CTACTTGTCCCCTGGTTCAGTAGAGGCCCCGGTTTCCCAGTTGTTGACTGTGACAGGCTC	5941 5941	Фр
5940 5940	CTGTGCTTTÄAATAAACAAATGTACCAAAAAACAAGTATCAAGCTGTTTAAGTGCTTCGG 	5881 5881	Qy Db
5880 5880	GCTTCACTGGAAATAATTTATTCATTGCAGATACTTTTTAGGTGGCATTTTATTCATTTC	5821 5821	Db Qy
5820 5820	CAAGCCCACCGGACATGGCCTTGGTAAAGGTTAGCAGACTGGTGTGTGT	5761 5761	Qу Дъ
5760 5760	AAGGGAAAGGTCTCAAGGAAGAGTCAACTGGGACAAGCA 	7	Qу
5700 5700	GCTCATCCACGTGGTCTGCCATGCCTACGAGGAAGGCCAGCGCATGCACGAGGACTGGTCTCT	5641 5641	Qу Db
5640 5640	TCAGGGTCACTGGAAACAGTGAAGTGCCATTTGTTGAAGCCTACTGCATGCCAGCCCACT	5581 5581	Qy Db
5580 5580	CCAGCCTGAGGAACCCTGGCTCTTTTCTTTAAAGCCCCAGGCCCACTTACATAAAACATT	5521 5521	Db Oy
5520 5520	TGGACAAGTTGCTGGCTCCTGAGACCAGTATTTCCTGGAGCTGTGCCTCAGTGAAGGGGC	5461 5461	ОУ
5460 5460	CACTGTTGCCTGCAAGGACACCACGTGGCCATTTTCCTTCAACTGAGGGCTCAAAACTCC	5401 5401	Db Qy
5400 5400	ATTCCACCCAAGGTGGGATTGGCCTTCCTTAGGCTGGCTACTTGTCACCATCACCGACAT	5341 5341	Оy
5340 5340	CCTCCATTCTCGACATTCCCCAACCTCCCAGCCCCTTCCAAGCAGGACTAGGTGCCCTGC	5281 5281	Db Oy
5280 5280	CTGCGGCTTCCTTCCCTCACTGAAGAGCCCTATTTGAATTCACTGTGTGGAGCCCTAGC	5221 5221	Db Qy
5220 5220	CCAGTGACCCTTGGCCTTGTGAGCCGAGATGCTGACCCTGCATAAAGGGCCAAAAGGAGGG	5161 5161	Db Db
5160 5160	TTAAGTCATGCCCTTGGCGTTGCCTATGGCACCTTTCCCTTCTGAAAGTCTGGTTCCTGC	5101 5101	Db Oy
5100 5100	TAGTCTCCTAAATGGCGTGTACTGCAAGACCTCTTGAACACTTTCCAGAGGATAGGATAT	5041 5041	ОУ
5040 5040	ATTCACCTTGGAAATGCACCGCCTĆAACTTGTTCACATGGCATAAATGAAAGGAATTTTA 	4981 4981	ДУ
4980 4980	CAATATTTCTGCGGCAAAAACTTCCTTCAAAAAATAAATGTACTTCATTGTATTCAATGA	4921 4921	ДЬ
4920	CCCTGCTCTGATCTGGAAGGAGGAGGGATTATGTTATAGCTTGTCAGCACAGTCCCCAAGTT	4861	Дb

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This invention describes a novel tumour-associated antigen, designated B345 which has cytostatic activity. B345 is involved in communication, interaction and/or signal transduction with extracellular components and ligands, especially in the metastatic potential of cancers, particularly of the colon. B345 or its immunogenic fragments, also the DNA that encodes it, are useful for immunotherapy of cancer, particularly carcinoma of lung or colon. Antibodies raised against B345 are useful for treatment and diagnosis of cancers that are associated with B345 expression, including their use for targeted delivery of cytotoxic or radioactive agents. Probes derived from B345 can be used to detect tumour-specific modulators. This sequence, and can be used to screen for B345 specific modulators. This sequence encodes a human B345 tumour-associated antigen described in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumour-associated antigen; human;
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                                                                                                                                                                     Example 6;
                                                                                                                                                                                        New tumor-associated antigen B345, useful immunotherapy of tumors, also related nucl
                                                                                                                                                                                                                                                                                        (BOEH ) BOEHRINGER INGELHEIM INT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ur-associated antigen; human; B345; cytostatic; cell communication; interaction; signal transduction; metastasis; cancer; colon; notherapy; carcinoma; lung; diagnosis; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGCATGGGCTCAGCAGATGCTGTCTTAATTTGTGGATGATACAGAAAGCCAGGCTTTGGG
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)B; AAM49640.
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 AGGGATCCTCCGGCTGCAGTTCCAAGTTTTGGTCCAACATCCACAAAATGAAAGCAATAA
                                                                                                                                           CTTCCCTGAGGATGAGCTCATGACGTGGCAGTTTGTCGTTCCTGCACACCTGCGGGCCAG
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                                     GAACATGGCGGGGAACTTCAACCTCTCTCTGCAAGGCTGTGACCAAGATGCCCAAAGTCC
                                                                                  CTACATCCCGGGCTCCACCACCACCCGAGCTGTTCAAGCTGGAGGACAAGCAGCCTGG
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                                                                                                                                CTTCCCTGAGGATGAGCTCATGACGTGGCAGTTTGTCGTTCCTGCACACCTGCGGGCCAG
                                                                                                                                                                                                                              CGAGTCTGTGTTTGAGGGTGAAGGCTCAGCAACCCTGATGTCTGCCAACTACCCAGAAGG
                                                                                                                                                                                                                                                                             CAGAAATGTCTCCGGCTTCAGCATTGCAAACCGCTCATCTATAAAACGTCTGTGCATCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGTCCTTTTGGGGAGGTTCAGCTTCAGCCCTCGACATCGTTGTTGCCTACCCTCAACAG
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99.9%;
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3203	CCAGAAAAGAATGTGTGTGTTTGAGCAGCATTGACACATATCTGCTTTGATAAGAGACTT	3144	Дb
3470	CAGAAAAGAATGTGTGTTTTGAGCAGCATTGACACATATCTGCTTTGATAAGAGACTT	3411	Оу
3143	ACCGCTAGATAAACGTGTGCCTGTCCCCCAGGTGGGGAATAATTTACAATCTGTCCAA	3084	Db
3410	CCGCTAGATAAACGTGTGCCTGTCCCCCAGGTGGTGGGGAATAATTTACAATCTGTCCAA	3351	Оу
3083	ACCTGACTTAGTAATAACTCATACTAACTGGTTTGGATGCCTGGGTTGTGACTTCTACTG	3024	Db
3350	CCTGACTTAGTAATAACTCATACTAACTGGTTTGGATGCCTGGGTTGTGACTTCTACTG	3291	Qy
3023	ATTTATTTGGTGGTCCTGTGTTATTTAAGAGAGATCAAATGTATAACCACCTAGCTCTTTTC	2964	Дb
3290	TTTATTTGGTGGTCCTGTGTTATTTAAGAGATCAAATGTATAAACCACCTAGCTCTTTTC	3231	Qy
2963	GAGGTCCCTACTCTCACTGGGGTCCCCAGGATGAAAACGACAATGTGCCTTTTTATTTA	2904	Db
3230	AGGTCCCTACTCTCACTGGGGTCCCCAGGATGAAAACGACAATGTGCCTTTTTATTATT	3171	Qy
2903	-	2844	Db
3170	GTGTTAAACAGAGGCTTGCCCTCTTCAGGACAACAGTTCCAATTCCAAGGAGCCTACCT	3111	Qy
2843	TAATGAGAGAGAGAGAGTCACCTAGCATAGGGTTGCAGCAAGCCCTGGATTCAG	2784	Db
3110	AATGAGAGGAGAGAGACCTGAGTCACCTAGCATAGGGTTGCAGCAAGCCCCTGGATTCAG	3051	Qy
2783	TGGATACAGTCATGACAGCTCATGTGCTCCTCAACTTAGGCTGTGCGGTTAGGCCAGCCTG	2724	Db
3050	GGATACAGTCATGACAGCTCATGTGCTCCTCAACTTAGGCTGTGCGGTTAGCCAGCC	2991	Qy
2723	TTCACATTGCTCAGTGGACTCATTCTAAGGGCAAGACATTGAAAATGATGAATTCCAATC	2664	ДЪ
2990	CACATTGCTCAGTGGACTCATTCTAAGGGCAAGACATTGAAAATGATGAATTCCAATC	2931	Qy
2663	TCCTAAAGAAGAGGAATTATACAGAAGGAACAGCAGGAGGTTTTCCTGGACACCGCCAAC	2604	Дb
2930	CCTAAAGAAGAAGAATTATACAGAAGGAACAGCAGGAGGTTTTCCTGGACACCGCCAAC	2871	Qy
60		54	Db -
2870	CTTTGCTGAGTTTCATAAAGCAGGGCACTGAGACACCCGTCCGT	2811	Qy
2543	TCCCTTACTGAACACTCAGGAGCCCATGGAGCCAGCAGAATAACTTGATCCATTCCAGAC	2484	Db
2810	CCCTTACTGAACACTCAGGAGCCCATGGAGCCAGCAGAATAACTTGATCCATTCCAGAC	2751	Qy
2483	TGAACCGTACACCTTCTCCCATCCCAACAATGGGGATGTAAGCAGCAGCAAGACAT	2424	фd
2750	GAACCGTACACCTTCTCCCATCCCAACAATGGGGATGTAAGCAGCAGGACACAGACA	2691	Qy
2423	CCCAACTGCAAAGTTGGCCACTGAGGAGCCACCTCCTCGCTCCCTGAGTCTGAGAG	2364	Db
2690	ссаастверала в торого в предержение в предержение в представля в предержение в предержение в представляющих в	2631	Qy
2363	GGGGGTCTGTCCTCCCCCACCCACCATATGCTCCAGGG	2304	фd
2630	CCGTTCCAGGGCACCATGGGGGTCTGTCCTCCCTCCCCACCCA	2571	Qy
2303	TGGGCATCTGCTACAGGATTCCAGCGGCTCCTTCCTGCAGCCAGAGGTGGACACCTACCG	2244	DЬ
2570	GGGCATCTGCTACAGGATTCCAGCGGCTCCTTCCTGCAGCCAGAGGTGGACACCTAC	2511	Qy
2243	GAAAGGGCGAAAGGACAATGACTCCCATGTGTATGCAGTCATCGAGGACACCATGGTATA	2184	Db
2510	AAAGGGCGAAAGGACAATGACTCCCATGTGTATGCAGTCATCGAGGACACCATGGTA	2451	Qy
2183	TGTGGGTATCTACAATGGCAACATCAATACTGAGATGCC-AGGCAGCCAAAAAAGTTTCA	2125	Дb
2450	GTGGGTATCTACAATGGCAACATCAATACTGAGATGCCGAGGCAGCCAAAAAAGTTT	2391	Qy

4610	TGGAGTGCAGTGGCGCAATCTCGGCTCACTGCAACCTCTGCCTCCTGGGCTCAAGCAATT	4551	Ş
4283	GCCTAGG	4224	₽
4550	TCTTTTTTCTTTTTTTTTTTTAATGTGAGACAGGATCTCATTCTGTTGCCTAGGC	4491	ð
4223	CTAATCAGGTGAGTAGACCATGAGACCAATGTGTGCTCACATTACCCTTTTTCTTTTTT	4164	Дb
4490	AGACCAATGTGTGCTCACATTACCCTTTTTCTTTTTT	4431	8
4430 4163	CTGATCAATGCCCCTGCAGGTTGCATTTATTGTAATGAAAAAAAA	4371	Db Qy
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4370	CACCACAGCCCACACTACGCCCTATCACTTCCCACAATGAGGCTAAGTGTTTTGTTTCTA	4311	Ş
4310	AACAACTGGCTTGGAGCTGGGCACCAGCTCTGCCTTTAGAAGGGGTGTCCACTTCACCAGG	3984	B &
98	TAAAAAACCCCAGATCAGAAGATCTGGCCATGCTGGGGGCTCACATTCTCACCTAGC	9	, B
4250	ACTTAAAAAAACCCCAGATCAGAAGATCTGGCCATGCTGGGGCTCACATTCTCACCTAGC	4191	Qy
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4190	GAGAGGCTACAAAATGATCTGGCGCACAGGGATGTTTTGTTTAGCTTGCGGACTCTAAC	4131	γ
4130 3863	AGGACATCTTTGGGGTGCTGTTATTCTGCCTACCACACCTTCCTGCCACTGACTCCCACA	4071 3804	p &
3803	CATCCTGGAAGAGCCTTTTGCCATGCAAGACAACATAGCCACAGGTGGGGATTAGGACC	. 3744	밁
4070	ACAACATAGCCACAGGTGGGGATTAGGACC	4011	Qy
4010 3743	TTTGACTTACAAAGCCCACCAGGAAGATCCAGGATAATCTCTCCATCTAAAGATCCTTCA	3951 3684	g dy
σ	GTGGCTGGTCAAGCTTTTCTCACATGGCATCACTGTGACACTGGCCCTCCCACTTCCCTC	62	90
3950	TGGCTGGTCAAGCTTTTCTCACATGGCATCACTGTGACACTGGCCCTCCCCACTTCCCTC	3891	ο
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3890	GAGAAGCCGGTTCCTTGCCATTTCAAGCTTCTAGAGGCTGGCT	3831	γQ
3563	SWALES INCLUSIVATIONAMATICANSSISTICASCASAGCTSTSCTTCTTSAAGGCTCTTAG [	3504	B 8
50	aCTTGGTAGCTTAAAAACAACACACTTAGCTTATAGTCCTGGGGATCAGAATTCCAAAAT	4 (	2 5
77	TACTTGGTAGCTTAAAAACACACATTAGCTTATAGTCCTGGGGATCAGAATTCCCAAAAT	71	5 5
3443	TTTAAATATATACCAAACAGTGGCCCCCTGCATTAGTTTTCTGTTGCCACTGCAACCCAT	3384	밁
3710	TAAATATATACCAAACAGTGGCCCCCTGCATTAGTTTTCTGTTTGCCACTGCAACCCAT	3651	Ωy
3383	TGCAGCAATACTTTGACATTTAAAGAGAAATTTAGAGAATATTCTCATCCTCTAAAAATG	3324	뭥
3650	GCAGCAATACTTTGACATTTAAAGAGAAATTTAGAGAATATTCTCATCCTCTAAAAATG	3591	Q
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3263	CTGATTCTCTAGGTCGGTTCGTGGTTATCCCATTGTGGAAATTCATCTTGAATCCCATT	3204	₽
3530	CCTGATTCTCTAGGTCGGTTCGTGGTTATCCCATTGTGGAAATTCATCTTGAATCCCATT		Q

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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                  Primer sets for synthesizing polynucleotides, purill-length cDNAs defined in the specification, and/or diagnosis of the abnormality of the proteinl-length cDNAs.
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i, Sugiyama
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T, Wakamatsu
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                                        polynucleotides, particularly the 5602 the specification, and for the detection rmality of the proteins encoded by the
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A, Nagai K,
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, Otsuki
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CC the 5602 nucleotide comprises at least 15 nucleotides; or the complementary to the comprises at least 15 nucleotides; or the complementary to the comprises at least 15 nucleotides; or the complementary to the comprises a 5'-end cc complementary strand of a polynucleotide which comprises a 5'-end cc polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence, where the coligonucleotide comprises a 3'-end sequence, where the cc oligonucleotide comprises at least 15 nucleotides and the combination of ct for 5'-end sequence/3'-end sequence is selected from those defined in cc the specification. The primer sets can be used in antisense therapy and cf in gene therapy. The primers are useful for synthesising polynucleotides, cc particularly full-length cDNAs. The primers are also useful for the cettion and/or diagnosis of the abnormality of the proteins encoded by cc the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and CAAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAH3633 represent human amino acid sequences; and AAH13629 to AAH13632 crepresent oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   comprises: (a) an oligo-dT primer and an oligonucle to the complementary strand of a polynucleotide which 5602 nucleotide sequences defined in the specific oligonucleotide comprises at a complementary strand of a polynucleotide which 5602 nucleotide sequences defined in the specific oligonucleotide comprises at a complementary strand of the specific of an artificial sequences are comprised as a comprise of an artificial sequences.
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Sequence 5573 BP; 1373 A; 1524 C; 1290 G; 1386 T; 0 other;

Qy Ş 밁 δÃ Вþ В δ В δ В Ωy В δÃ 밁 δ ₽ δĀ В δÃ В 20 Query Match Best Local Sim. Matches 5566; 1049 540 480 420 569 989 360 929 300 869 608 180 121 629 240 749 689 61 ب TTCCTGCACACCTGCGGGCCAGCGTCTCCTTCCTCAACTTCAACCTCTCCAACTGTGAGA 1108 TACACCTCCCATGGTTCCACCCCAGAAATGTCTCCGGCTTCAGCATTGCAAACCGCTCAT CCTTCTGCAGCAATGGCACTGTGTCCCGGATCAAGATGCAAGAAGAGGAGTGAAAATGGCCT TACACCTCCCATGGTTCCACCCCAGAAATGTCTCCGGCTTCAGCATTGCAAAACCGCTCAT CAGACGGAGTCACTCCATCAGCGGCCGAATCGATGCCACCGTGGTCAGGATCGGAA CAGACGGAGTCACTCCATCAGCGGCCGAATCGATGCCACCGTGGTCAGGATCGGAA CTATAAAACGTCTGTGCATCATCGAGTCTGTGTTTGAGGGTGAAGGCTCAGCAACCCTGA CCTTCTGCAGCAATGGCACTGTGTCCCGGATCAAGATGCAAGAAGGAGTGAAAATGGCCT CGTTGTTGCCTACCCTCAACAGAACTTTCATCTGGGATGTCAAAGCTCATAAGAGCATCG Similarity Conservative 99.5%; 0, Score 5518.4; Pred. No. 0; Mismatches DB 6, 22; Length 4; Gaps 479 1048 419 988 928 299 868 239 808 179 748 120 889 4.

2308 1739	2249 CGGTGACACTTACCCCAAGGACTGTGGACTTGACTGTCATCCCCATCGCAGCGGTGGGAG	D 09
2248 · 1679	2189 TCTGGGTCAACATCTCTAACTGCAGCCCCACGAGCGCAAGCAGCTAGACCTGCTCTTCT*	Db Oy
2188 1619	2129 AGGAGATCTTCAGCCTGGACGAGGGATGTGCTCCCCAAGCCAAGCTTCCACCATCACAGCT	p oy
2128 1559	2069 GCGTGGTCTGCCAGACAGGGCGCGCATTCATGATCATCCAGGAGCAGCGGACCCGGGCTG	p Q
2068 1499	2009 GGAACATCAGCGTGCCCAGAGACCAGGTGGCCTGCCTGACTTTCTTT	рь
2008 1439	1949 AGGTCTACCTGAGGACCCCCAACTGGGACCGGGGCCTGCCATCCCTCACCTCTGTGTCCT	p oy
1948 1379	1889 CCTTTATACCTTATTTCAAAGAGGAAGGCGTTTTCACGGTGACCCCTGACACAAAAAGCA 	pb Qy
1888 1319	1829 CCCTTCGCACCTTTGCCCCCAGCTTCCAACAAGAGGCCTCCAGGCAGG	Db Qy
1828 1259	.1769 GCTCCTTCTGCCCGGGAGGCTCTATCAAGCAGATCCAGGTGAAGCAGAACATCTGGGTGA	D Q
1768 1199	1709 GCAACACCAGCTTCAGCTACCTCGTGGCCAGTGCCATACCCAGCCAG	D Qy
1708 1139	1649 GGCTCAGCCTGGTGCTGGTGCCAGCCCAGAAGCTGCAGCAGCAGCATACACACGAGAAAGCCCT 	p Q
1648 1079	1589 TCCTCCACCTGCCTGTGGAGCTGCATGACTTCTCCTGGAAGCTGCTGGTGGTGCCCAAGGACA 	р <i>9</i>
1588 1019	1529 GCTGCACAGACCACCGGTACTGCCAAAGGAAATCCTACTCACTC	D Q
1528 959	1469 ARATCTCCTTCCTTTGTGATGATGATGACACGTCTGTGGATGAATGTGGAAAAAACCATAA 	Db Oy
1468 899	1409 TGTGTCTAGAATCTCGGACCTGCAGTAGCAACCTCACCCTGACATCTGGCTCCAAACACA	Db Qy
1408 839	1349 CACTCACCATCGAGCCACGGCCCGTCAAACAGAGCCGCAAGTTTGTCCCTGGCTGTTTCG	Db Qy
1348 779	1289 ATCCACAAATGAAAGCAATAAAATCTACGTGGTTGACTTGAGTAATGAGCGAGC	ру
1288 719	1229 GTGACCAAGATGCCCAAAGTCCAGGGATCCTCCGGCTGCAGTTCCCAAGTTTTGGTCCAAC	pb 99
659	00 AGCTGGAGGACAAGCAGCCTGGGAACATGGCGGGGAACTTCAACCTCTCTCT	В

Qy Db	p Qy	Qy Qy	ממ	Qy	0y 0y	оу оу оу	оу оу оу	0	04 pp		Q D D Q D D Q D D Q Q D D Q Q D D Q Q D		Q D Q D Q D Q D Q D Q Q D Q Q Q Q Q Q Q	Q	Q B Q B Q B Q B Q B Q B Q B Q B Q Q Q Q	Q B Q B Q B Q B Q B Q B Q B Q B Q Q B Q	Q B Q B Q B Q B Q B Q B Q B Q B Q Q B Q
3329 G       2760 G	3269 G 1 2700 G	3209 2640		3149 2580	3089 2520 3149 2580	3029 3089 3520 3149	2969 2400 3029 2460 3089 2520 3149	2909 2340 2969 3029 3029 3089 3149	2849 2909 2909 2969 2969 3029 3029 3089 3149	2789 2849 2909 2940 2969 2460 3029 3149	2729 2160 2789 22849 2280 22909 2340 23400 3089 3149	2669 2729 2729 2789 2789 22849 22909 23969 23089 3149	2609 2669 2729 2160 2789 22849 22849 22969 2340 3089 3149	2549 1980 2609 2609 27040 27100 27729 2789 22849 22849 23400 3089 3149	2489 1920 2549 2569 2669 27100 27729 2789 22849 22849 23400 3089 3149	2429 11860 2489 12549 25609 2669 27729 27729 2789 22849 22969 23089 3149	2369 1800 2429 1980 2549 1990 2669 27729 2789 2789 22849 23400 3089 3149
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	TATAACCACCTAGCTCTTTTCACCTGACTTAGTAATAACTCATACTAACTGGTTTGGAT 	CCTTTTTATT.	TCCAATTCCAAGGAGCCTACCTGAGGTCCCTACTCACTGGGGTCCCCAGGATGAAAAC 		TGCAGCAAGCCCTGGATTCAGAGTGTTAAACAGAGGCTTGCCCTCTTCAGGACAACAG 	GCGGTTAGCCAGC                      	GATGAATTCCAATCT	GTTTTCCTGGACACCGCCAACTTCACATTGCTCAGTGGACTCATTCTAAGG	GTGTTCCTAACCAGAAATCCTAAAGAAGAGAATTATACAGAAGAACACIIIIIIIIII	TGATCCATTCCAC	NAGCAGGAAGGACACAGACATTCCCTTACTGAACACTCAGGAGCCCATGGAGCCA NAGCAGGACGAAGGACACAGACATTCCCTTACTGAACACTCAGGAGCCCATGGAGCCA NAGCAGCAAGGACACAGACATTCCCTTACTGAACACTCAGGAGCCCATGGAGCCA ATAACTTGATCCCATTCCAGACGCTTTGCTGAGATTTCATAAAGCAGGGCACTGAGA ATAACTTGATCCATTCCAGACGCTTTGCTGAGATTTATACAGAAGGAACACA ATAACTTGATCCATTCCAGACGCTTTGCTGAGATTATATACAGAAGGAACAGC GTCCGTGTTCCTAACCAGAAATCCTAAAGAAGAAGGAATTATACAGAAGGAACAGC GTCCGTGTTCCTGACCAGAAATCCTAAAGAAGAAGGAATTATACAGAAGGAACAGC GTTTTCCTGGACACCAGCAACTTCACATTGCTCAGTGGACTCATTCTAAGGGCAA GTTTTCCTGGACACCGCCAACTTCACATTGCTCAGTGGACTCATTCTAAGGGCAA HILLIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI	CTCCCCTCCTGAGTCTGAGAGTGAACCGTACACCTTCTCCCATCCCAACAATG	ACCCACCATATGCTCCAGGGCCCCAACTGCAAAGTTGGCCACTGAGGAGCCACCTCCTCACCACCACACATATGCTCCAGGGGCCCCAACATTGGCCAACATTGGCCACCTCCTCACCACACATATGCTCCAGGGGCCCCAACATGCAAAAGTTGGCCACCTGCAGGAGCCACCTCCTCCCCCCCC	AGCCAGAGGTGGACACCTACCGGCCGTTCCAGGGCACCATGGGGGTCTGTCCTCCCTC	ACACCATGGT.	GAGGCAGCAAAAAAGTTTCAGAAAGGGCGAAAGGACAATGACTCCCATGTGTATGCAGGAGGACACCAAAAAAAGTTTCAGAAAGGGCGAAAGGACAATGACTCCCATGTGTATGCAGGAGGACACCAAAAAAAA	ACAAGGCCCC ACAAAAAGTT CCAAAAAAGTT ACACCATGGT ACACCATGGT ACACCATGGT ACACCATGGT ACACCATGGT ACACCATGGT ACACCATGGT ATGGACACCTA ATGGACACCTA ATGGACACCTA ATGGACACCAGA AGGACACCAGA ATGCATTCCA AGGACACCAGC ATGAATTCCA AGGACACCAGC AGGCCCTGGATT AGCCCCTGGATT AGCCCTGGATT AGCCCCTGGATT AGCCCCTGGATT AGCCCCTGGATT AGCCCCTGGATT AGCCCTGGATT AGC
	TTCACCTGA	PATTATTTAT	ACCTGAGGTC            ACCTGAGGTC		CAGAGTGTT	AGCCTGTAATGAGAGG	NATCTGGATA           NATCGGGATA CTGTAATGA             CTGTAATGA CTGTAATGA           CTGTAATGA	PARCTTCACA             AACTTCACA 	AAAATCCTAA            AAACTTCCTAA   AACTTCACA   AACTTCACA   AATCTGATCACA           AATCTGGATA             CAGAGTGTT   CAGAGTGTTTCAGAGTGTTTCAGAGTGTTTCAGAGTGTTTCAGAGTGTTTTTCAGAGTGTTTTTCAGAGTGTTTTCAGAGTGTTTTCAGAGTGTTTTCAGAGTGTTTTCAGAGTGTTTTCAGAGTGTTTTCAGAGTGTTTTCAGAGTGTTTTCAGAGTGTTTTCAGAGTGTTTTCAGAGTGTTTTCAGAGTGTTTCAGAGTGTTTCAGAGTGTTTTCAGAGTGTTTTCAGAGAGTGTTTTCAGAGTGTTTTCAGAGTGTTTTCAGAGAGTGTTTTCAGAGTGTTTTCAGAGTGTTTTCAGAGTGTTTTCAGAGTGTTTTCAGAGTGTTTTCAGAGTGTTTTCAGAGTGTTTTCAGAGTGTTTTCAGAGTGTTTTTCAGAGTGTTTTTCAGAGTGTTTTCAGAGTGTTTTCAGAGTGTTTTCAGAGTGTTTTCAGAGTGTTTTCAGAGTGTTTTCAGAGTGTTTTCAGAGTGTTTTCAGAGTGTTTTCAGAGTGTTTTTCAGAGTGTTTTCAGAGTGTTTTCAGAGTGTTTTTCAGAGTGTTTTTCAGAGTGTTTTTCAGAGTGTTTTTTCAGAGTGTTTTTTCAGAGTGTTTTTTCAGAGTGTTTTTTTT	CAGACGCTTTGCTO AGAAATCCTAAAGJ AGAAATCCTAAAGJ CAAACTTCACATTC CAAACTTCACATTC CAAACTTCACATTC CAAACTTCACATTC CAAACTTCACATTC CAAACTTCACATTC CAAACTTCACATTC CAAATCTTCACATTC CAAATCTTCACATTC CAAATCTTCACATTC CAAATCTTCACATTC CAATCTGGATACAC CAATCTGGATACAC CAATCGGGATACAC CAATCGGAATCGTAAAC CAATCACACAC CAATCACACACAC CAATCACACACA	ACATTCCCTI ACATTCCCTI ACACCCTTTG ACACCCTTTG ACACCCTTTG ACACCCTAA ACCTTCACA IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	GAGTGAACC	GGCCCCAAC             GGCCCCAAC   GAGTGAACO   GAGTGAACO   GAGTGAACO	ACCEGCCETY ACCEGCCETY ACCEGCCCAAC ACATTCCCTA ACATTCCCTA ACATCCTTA ACATCCTTA ACATCCTTA ACATCCTTA ACATCCTAA ACTTCCTA ACATCCTAA ACTTCAA ACTTCAA ACTTCAA ACTTCACA ACTTCAC	PATATGGCA	TCAGAAAGG TTCAGAAAGG TTCAGAAAGG TTTTTTTTTT	CGCTGTGGG CCCTTGTGGG CTTTCAGAAAGG CTTTCAGAAAGG CTTTTCAGAAAGG CTTTTCAGAAAGG CTTTTCAGAAAGG CCGGCCGTT CAGTGCCCAC CAGTGCAACA CAGTGCAACA CAGTGCAACA CAGTGCAACA CAGTGCATTCAAACA CAGTTCCTTA CAGTTCCTTA CAGTTCCTTA CAGTTCCTTA CAGTTCCTAA CAGTTCCTAA CAGTTCCTAA CAGTTCCTAA CAGTTCCTAA CAGTTCCTAA CAGTTCCTAA CAGTTCCTAA CAGTTCCTAA CAGTTCACAA CAGTTCACAA CAGTTCACAA CAGTTCACAA CAGTTCACAA CAGTTCACAA CAGTTCACAA CAGTTCACAA CAGTTCACAA CAGTTCACAA CAGTTCACAA CAGTTCACAA CAGTTCACAA CAGTTCACAA CAGTTCACAA CAGTTCACAA CAGTTCACAA CAGTTCACAA
PAGATAAACG	ACTTAGTAAT	rrreereere             rreereere	CCTACTCTC CCTACTCTC		TAAACAGAGG              TAAACAGAGG	AGAGGAGAGA            AGAGGAGAGA  AAACAGAGG	TGGATACAGTCATGACAG	ATTGCTCAGT ATTGCTCAGT ATTGCTCATGA CCAGTCATGA CAGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	AAGAAGAGGA AAGAAGAGGA AATTGCTCAGT IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	SCTGAGTTTC	PACTGAACAC	GFACACCTY            DGTACACCTY	TIGCAAAGTI            TIGTACACATI TIGTACACCTI TACTGAACAC             TACTGAACAC              TAGAAGAGAGA              	CCAGGGCAC  CCAGGGCAC  CCAGGGCAC  CCAGGGCAC  CCAGGGCAC  CCAGGCAC  CCAGCCAC  CCAGGCAC  CCAGCCAC  CCAGGCAC  CCAGCCAC  CCAGGCAC  CCAGCCAC  CCAGGCAC  CCAGCAC  CCAGGCAC  CCAGGCAC  CCAGGCAC  CCAGCCAC  CC	ATCTGCTACA IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	GCGAAAGGA GCGAAAGGA GCGAAAGGA IIIIIIIIII	TRATCTACAA IIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
CCTGGGTTGTGACTTCTACTGACCGCTAGATAAACGTGTGCCTGTCCCCCAGGTGGTG	FAACTCATA	CTGTGTTA	CACTGGGGT	CTTGCCCT	CTTGCCCT	AGAGAGGCCTGAGTC	ACAGCTCATON ACAGCTCATON ACAGCTCATON ACAGCCTGAGAGAGAGCCCGAGAGAGGCCCGAGAGAGCCCTON ACAGCCCCTON ACAGCCCTON ACAGCCCCTON ACAGCCCCCTON ACAGCCCCTON ACAGCCCCCTON ACAGCCCCTON ACAGCCCCTON ACAGCCCCCTON ACAGCCCCCTON ACAGCCCCCTON ACAGCCCCCTON ACAGCCCCTON ACAGCCCCCTON ACAGCCCCCTON ACAGCCCCTON ACAGCCCCTON ACAGCCCCTON ACAGCCCCTON ACAGCCCCTON ACAGCCCCCTON ACAGCCCCCTON ACAGCCCCTON ACAGCCCCCTON ACAGCCCCCTON ACAGCCCCCTON ACAGCCCCCCTON ACAGCCCCCTON ACAGCCCCCCTON ACACCCCCCCTON ACACCCCCCCTON ACACCCCCCTON ACACCC	RGGACTCAT"	AATTATACA           AATTATACA 	GAGTTTCATAAAGCAGGGCACTGAGAC GAGTTTCATAAAGCAGGGCACTGAGAC GAGTTTCATAAAGCAGGGGCACTGAGAC AAGAAGGAATTATACAGAAGGAACACACA	TCAGGAGC TILLILI TILLILI TATAAAGCA TATAAAAGCA TATAAAGCA TATAAAAGCA TATAAAGCA TATAAAGCA TATAAAGCA TATAAAGCA TATAAAGCA TATAAAAGCA TATAAAGCA TATAAAGCA TATAAAAGCA TATAAAAAAAAAA	reteccate	IGGCCACTG	CATGGGGG	AGGATTCCAN AGGATTCCAN AGGATTCCAN AGGATTCCAN CATGGGGG CATGGGGGG CATGGGGGG CATGGGCCACTG AGGCCACTG AGGCCACTG AGGCCACTG AGGCCACTG AGGCCACTG AGGCCACTG AGGCCACTG AGGCCACTG AGGCCATCA AGGCCTCAT AGGCCCAT ACAGCTCAT A	ACAATGACTULILILILILILILILILILILILILILILILILILILI	ATGGCACACA ATGGCACACA AGATTACACA AGATTATACACA AGATTATACACA AGATTATACACA AGATTACACAT ACAGCTCAT ACAGCTC
TCCCCCAGG	CTAACTGG1	TTTAAGAG!            TTAAGAG!	CCCCAGGAT		CTTCAGGAC	TCACCTAGCATI	SCTCATGTGCTCCACCTT	TCTAAGGG          TCTAAGGGG	GAAGGAACA [	GGGCACTGA GGGCACTGA GGGCACTGA GGAAGGAACA GAAGGAACA TCTAAGGACA TCACCTAGC	CCATGAGG CCATGAGG CCATGAGG CCATGAGGG CGGGGACTG GGGCACTG GGAGGAACA [          GGAGGAACA TCTAAGGGG	CCAACAATG  CCAACAATG  CCATGAGACG  CCATGGAGC  GGGCACTGA             GGGCACTGA              GGGCACTGA              GGGCACTGA  GAAGGAACA               GTCTAAGGGA  TCTAAGGGC  TCTCACGTAG  GTGCTCCTC  TCACCTAGG              TCACCTAGG  TCACCTAGGAC  TCACCTAGGAC  TCACCTAGGAC  TCACCTAGGAC  TCACCTAGGAC	AGGAGCCAC AGGAGCCAC CCACACATE           CCAACACATE             CCATGACACE             CCATGACACE             CCATGACCTCA GGGCACTCA             GGGCACTCA             GGGCACTCA GAAGGAACA            GGAGGAACA	TCTGTCCTC IIIIIIIIIIIIIIIIIIIIIIIIIIIIII	GCGGCTCCT GCGGCTCCT GCGGCTCCT TCTGTCCTC TCTGTCCTC AGGAGCCAC HILLIIII AGGAGCCAC CCAACAATG CCAACAATG CCAACAATG CCATGAGG GGCACTGA GGCACTGA HILLIIII GGGCACTGA HILLIIIII GGAAGGAACA HILLIIIIIIII GGAAGGAACA HILLIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	CCCATGTGT	TCAATACTE
GTGGTGG	TTTGGAT         TTGGAT	ATCAAAT         ATCAAAT	TGAAAAC         TGAAAAC	CAACAGT		CATAGGG          CATAGGG	CAACTTA          CAACTTA CATAGGG 	GCAAGACA GCAAGACTTA HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	AGCAGGA           AGCAGGA  CAAGACA           CAACTTA          CATAGGG  CATAGGG	AGACACC AGACACC AGACACAC AGCAGACACACACAC	CCAGCAG	GGGGATG GGGGATG CCAGCAG AGACACC AGACACC IIIIII AGACACCC AGCAGGA IIIIIII AGCAGGA AGCACACC AGCAGGA AGCACACC AGCAGGA AGCACACC AGCAGGA AGCAGGACA AGCAGGACA AGCAGGACA AGCAGGACA AGCAGGACA AGCAACTTA CCAACTTA CCAACTTA CCAACTTA CCAACTTA CCAACTTA CCAACTTA CCAACTTA CCAACTTA	CCTCCTC CCTCCTC CCTCCTC CCTCCTC GGGGATG GGGATG GCAGCAG CCAGCAG AGACACC AGACACC AGACACC AGACACC AGACACC AGACACC AGACACC AGACACC AGCAGCAG AGACACC AGCAGCAG AGCAGCA AGCAGCA AGCAGCA AGCAGCA AGCAGCAC AGCAGCAGC AGCAGCAGC AGCAGCAGC AGCAGCAGC AGCACTTA CCAACTTA CCAACTTA CCAACTTA CCAACTTA CCAACTTA	CCCTCCC CCTCCCC CCTCCTCC CCTCCTCC CCTCCT	TTCCTGC TTCCTGC CCTCCTCC CCTCCTCCC CCTCCTCC CCTCCTCC CCTCCT	TATGCAG TATGCAG TATGCAG TATGCAG TICLIC CCTCCTCC CCTCCTCC CCTCCTC CCTCCTC CCTCCT	GAGATGC GAGATGC GAGATGC GAGATGC TATGCAG TATGCAG TATCCTGC CCCTCCCC CCCTCCCC CCCTCCCC CCCTCCCC CCCTCCCC CCCTCCCC CCCTCCCC CCCTCCT
3388 2819	3328 2759	3268 2699	3208 2639	3148 2579	2519	3088	08	96	96 96 96 96 96	2848 2279 2908 2339 2339 2968 2399 3028 2459	2768 2219 2848 2279 2908 2339 2968 2339 3028 3088	2728 2159 2788 2219 2848 2219 2848 2279 2908 2339 2968 2339 3028 3088	2668 2099 2728 2159 2178 2219 2219 22279 2908 2339 2968 2399 3028	2608 2039 2668 2099 2728 2159 27788 2219 2219 22848 22279 2339 2908 2339 3088	2548 1979 2608 2039 2668 2099 2728 2728 2728 2788 22159 2788 22219 2848 2239 2908 2339 2968 2339 3028	2488 1919 2548 1979 2608 2039 2668 2099 2728 2159 27788 2219 22788 2219 2339 2848 22399 3028 3088	4 8 4 9 7 9 0 0 0 7 1 7 2 8 2 9 8 9 8 0 4 0

4527	TCACATTACCCTTTTTCTTTTTTTTTTTTTTTTTTTTTT	4468	Qy
4467 3899	AAAAAGAAAGACTIGGGATTAATCTCTAATCAGGTGAGTAGACCATGAGACCAATGTGTGC	3840	B 5
	AGGCTAAGTGTTTGTTTCTACTGATCAATGCCCCTGCAGGTTGCATTTATTGTAAT	78	B
	ATGAGGCTAAGTGTTTGTTTCTACTGATCAATGCCCCTGCAGGTTGCATTTATTGTAATG	ω 4-	Ş
4347	GAAGGGGTGTCCACTTCACCAGGTCACCACAGCCCACACTACGCCCTATCACTTCCCACA	4288	98
3779		3720	64
4287	TGGGGCTCACATTCTCACCTAGCAACAACTGGCTGGAGCTGGGCACCAGCTCTGCCTTTA	4228	유
3719		3660	양
4227	TGTTTAGCTTGCGGACTCTAACACTT-AAAAAACCCCAGATCAGAAGATCTGGCCATGC	4169	β
3659		3600	64
4168	CTTCCTGCCACTGACTCCCACAGGAGAGGCTACAAAATGATCTGGCGCACAGGGATGTTT	4109	P
3599		3540	O
4108	GCCACAGGTGGGGATTAGGACCAGGACATCTTTGGGGTGCTGTTATTCTGCCTACCACAC	4049	do
3539		3480	Vo
4048	CTCTCCATCTAAAGATCCTTCATCATCCTGGAAGAGCCTTTTGCCATGCAAGACATA	3989	Qy
3479		3420	Db
3988	CACTGGCCCTCCCACTTCCCTCTTGACTTACAAAGCCCACCAGGAAGATCCAGGATAAT	3929	β
3419		3360	6
3928	CTGGCTGCATTCCCAGGCTCCAGTGGCTGGTCAAGCTTTTCTCACATGGCATCACTGTGA	3869	g
3359		3300	Q
3868	GTGCTCCTTCTGAAGGCTCTAGGGAGAAGCCGGTTCCTTGCCATTTCAAGCTTCTAGAGGIIIIIIIIII	3809	g
3299		3240	Q
3808 3239	CTGGGGATCAGAATTCCAAAATGGATGTCCCTGAATGAAAATCAAGGTGTCAGCAGAGCT 	3749 3180	дь Оу
3748	TTCTGTTGCCACTGCAACCCATTACTTGGTAGCTTAAAAACAACACATTAGCTTATAGTC	3689	dg
3179		3120	VQ
3688	ATATTCTCATCCTCTAAAAATGTTTAAATATATACCAAACAGTGGCCCCCTGCATTAGTT	3629	д
3119		3060	9
3628	TTCCATGTGCGGTTCTCCTAGCTGCAGCAATACTTTGACATTTAAAGAGAAATTTAGAGA	3569	gb
3059		3000	Qy
3568	GAAATTCATCTTGAATCCCATTGTCCTATAGTCCTAGCAATAAGAGAAAATTTCCTCAAGT	3509	å
2999		2940	S
3508	TATCTGCTTTGATAAGAGACTTCCTGATTCTCTAGGTCGGTTCGTGGTTATCCCATTGTG	3449	g
2939		2880	S
3448	GAATAATTTACAATCTGTCCAACCAGAAAAGAATGTGTGTG	3389	å
·2879		2820	S

07	TTTAAAGCCCAGGCCCCACTTACATAAAACATTTCAGGGTCACTGGAAACAGTGAAGTGC 56	5548	Qy
77	GTATTTICCTGGAGCTGTGCCTCAGTGAAGGGCCCAGCCTGAGGAACCCTGGCTCTTTTC 55	4918	Db Qg
17	CCATTTCCTTCAACTGAGGGCTCAAAACTCCTGGACAAGTTGCTGGCTCCTGAGACCA 49	85	Db
87	CCATTTTCCTTCAACTGAGGGCTCAAAACTCCTGGACAAGTTGCTGGCTCCTGAGACCA 54	5428	Qy
57	GGCTGGCTACTTGTCACCATCACCGACATCACTGTTGCCTGCAAGGACACCACGTG 48	79	Db
27	TTAGGCTGGCTACTTGTCACCATCACCACATCACTGTTGCCTGAAAGGACACCACGTG 54	י פ	O 10
67	CCCTTCCAAGCAGGACTAGGTGCCCTGCATTCCACCCAAGGTGGGATTGGCCTTC 53	5308	P 29
38	CCTTATTTGAATTCACTGTGTGGAGCCCTAGCCCTCCATTCTCGACATTCCCCAACCTC 47	4679	DЬ
07	TTATTTGAATTCACTGTGGAGCCCTAGCCCTCCATTCTCGACATTCCCCAACCTC 53	5248	Qy
78	GATGCTGACCCTGCATAAAGGGCCAAAGGAGGCCTGCGGCTTCCCTTCACTGAAGAG 46	4619	Db
47	ATGCTGACCCTGCATAAAGGGCCAAAGGAGGGCTGCGGCTTCCCTTCCCTCACTGAAGAG 52	5188	Qy
μ.		55	Db :
87	GCACCTTTCCCTTCTGAAAGTCTGGTTCCTGCCCAGTGACCCTTGGCCTTGTGAGCCGA 51	5128	Qy
58	AGTCATGCCCTTGGCGTTGCCTAT 45	4499	Db
27	ACCTCTTGAACACTTTCCAGAGGATAGGATATTTAAGTCATGCCCTTGGCGTTGCCTAT 51	5068	Оу
9	TTCACATGGCATAAATGAAAGGAATTTTATAGTCTCCTAAATGGCGTGTACTGCAA 44	3 0	Db 45
ת	TTUTTO AT COTTO TO THE A A COTTO TO THE TTUTTE A A COTTA A A COTTO TO	3	0
38		4379	DЬ
07	AAAAAATAAATGTACTTCATTGTATTCAATGAATTCACCTTGGAAATGCACCGCCTCAA 50	4948	Qу
78		4319	ממ
47	TATGTTATAGCTTGTCAGCACAGTCCCAAGTTCAATATTTCTGCGGCAAAAACTTCCTT 49	4888	Qy
118	CCCAGTAACTGTGGACTTTTGCTTCCTCACCCCTGCTCTGATCTGGAAGGAGGAGGGA 43	4259	Db
87	TGCCCAGTAACTGTGGACTTTTGCTTCCTCACCCCTGCTCTGATCTGGAAGGAA	4828	Qy
58	CCCCACACCCTCATTTATACCAATTAC 42	4199	рь
27	CTGGGATTACAGATGTGAGCCACCGCATCCAGCCCCACACCCTCATTTATACCAATTAC 48	4768	Qy
.98	CAGGCTGGTCTCAACCTCCTGGGCTCAAGCAATCCTCCTGCCTCGGCCTCCCAAAGT 41	4139	Дb
67	CCCAGGCTGGTCTCAACCTCCTGGGCTCAAGCAATCCTCCTGCCTCGGCCTCCCAAAGT 47	4708	Qy
138	A-TTTTTGTAGAGACAGGGTTTCACCATGTT 4	4080	дb
07	ACAAACCACCATGCCCAGCTAATTTTGTATTTTTTTTTT	4648	Qy
7		02	Db .
47	TGCCTCCTGGGCTCAAGCAATTCTCCCCACCTCAGCCTCCCAAATAGCTGGGATCACTGG 46	4588	ΟV
<u> </u>	GGATCTCATTCTGTTGCCTAGGCTGGAGTGCAGTGGCGCAATCTCGGCTCACTGCAACCT 40	3960	DB 45
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16-MAY-2000;
17-MAY-2000;
17-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; purified secretory polypeptide; cell proliferative disorder; ss cancer; immune system disorder; neurological disorder; mental disorder motor neuron disorder; demyelinating disorder; neuromuscular disorder; central nervous system disorder; enzyme linked immunosorbent assay;
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Sequences AAS63145-AAS63223 represent DNA encoding purified secretory CC polypeptides of the invention. The polypeptides and polynucleotides can be used in the treatment, prevention and diagnosis of diseases associated CC with inappropriate secretory protein expression. These diseases include CC cell proliferative disorders such as atherosclerosis and psoriasis, CC cancers such as leukaemia and melanoma, immune system disorders such as casthma and diabetes mellitus, neurological disorders such as epilepsy and CC parkinson's disease, mental disorders such as schizophrenia and seasonal CC lateral sclerosis, demyelinating disorders such as amyotrophic CC lateral sclerosis, demyelinating disorders such as multiple sclerosis, central nervous system disorders such as multiple sclerosis, CC neurofibromatosis and neuromuscular disorders such as cerebral palsy and CC neurofibromatosis and neuromuscular disorders such as cerebral palsy and CC neurofibromatosis and neuromuscular disorders such as mental retardation and CC muscular dystrophy. Target polynucleotides in a sample can be detected by hybridising the sample with a probe sequence complementary to the target CC polynucleotide, under conditions in which a hybridisation complex is CC polypeptides may also be used as antigens in the production of antibodies against secretory proteins and in assays to identify modulators of CC against secretory proteins and in assays to identify modulators of complex in expression and activity. The antibodies may also be used as cCC invention in samples e.g. by enzyme linked immunosorbent assay (ELISA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Panzer SR, Spiro PA, Banville SC, Shah P, Chalup MS, Char Chen A, D'sa SA, Amshey S, Dahl CR, Dam TC, Daniels SE; Dufour GE, Flores V, Fong WT, Greenawalt LB, Hillman JL, Liu TF, Roseberry AM, Rosen BH, Russo FD, Stockdreher TK, Wright RJ, Yap PE, Yu JY, Bradley DL, Bratcher SR, Chen Wichen HJ, Hodgson DM, Lincoln SE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis
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Query Match Best Local Local Similarity hes 3068; Conserv Conservative 39.1%; Score 2409.8; Pred. No. 0; 0; Mismatches 0; 153; DB 22; Indels Length 77; Gaps 49;

Sequence 3301 BP; 808

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AAACCA TGCCCA
AACACAAAATC           AACACAAAATC
GECGAGCCATGTCACTCAC
CAAGGCTGTGACCAAGATG
AGAGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
3-ATGTCTGCCAACTAC 
TACACCTCCCATGG
TCTGCAGCAATGG           TCTGCAGCAATGG
TAGAGCTGCAGTT ACGGAGTCACTCA 
TTAGAGCTGCAGTTT

2830	GCCCATGGAGCCAGCAGAATAACTTGATCCATTCCAGACGCTTTGCT-GAGTTTCATAAA	2772	Qy
2643	CCCAACAATGGGGATGTAAGCAAGCAAGGACACAGACATTCCCTTACTGAACACTCAGGA	2584	Db
2771	CCAACAATGGGGATGTAAGC-AGCAAGGACACAGACATTCCCCTTACTGAACACTCAGG	2713	Qy
2583	GAGGAGCCACCTCCTCGCTCCTGAGTCTGAGAGTGAACCGTACACCTTCTCCCAT	2524	Db
2712	AGGAGCCACCTCCTCGCTCCCTGAGTCTGAGAGTGAACCGTACACCTTCTCCC	2653	Qy
2523	TCCCCACCCATATGCTCCAGGGCCCCAACATGCAAAGGT	2464	рb
2652	TCCTCCC-TCCCCACCCACCATATGCTCCAGGGCCCCAACTGCAAAGTTGGCCAC	2597	Qy
2463	CCAGAGGTGGACACCTACACGGCCGTTCCAG	2404	Db
2596	CTTCCTGCAG-CCAGAGGTGGACACCTAC-CGGCCGTTCCAGGGC-ACCATGGGGGTC	2540	Qy
2403	TGCAGTCATCGAGGACACCACATGGTATAATGGGCATCTGCTACAGGATTCCATGCGGCT	2344	Db
2539	GCAGTCATCGAGGACACCATGGTATATGGGCATCTGCTACAGGATTCCA-GCGGC	2484	Qy
2343	GATGCCGAGGCAGAAAAAGTTTCAGAAAGGGCGAAAGGACAATGACTCCCATGTGTA	2284	Db
2483	ATGCCGAGGCAGCCAAAAAAGTTTCAGAAAGGGCGAAAGGACAATGACTCCCATGTGT	2424	Qy
2283	GAAAAAGAAGACAAACAAGGGCCCCGCTGTGGGTATCTACAATGGCAACATCAATACTGA	2224	Db
2423	AAAAAGAAGACAAACAAGGGCCCCGCTGTGGGTATCTACAATGGCAACATCAATACTG	2364	Qy
2223	GAGGTGGAGTCTTACTGCTGTCTGCCCTCGGGCTCATTCAT	2164	Db
2363	GAGGTGGAGTCTTACTGCTGTCTGCCCTTCGGGCTCA-TCATTTGCTGTGAAAAAG	2305	Qy
2163	TTCTCGGTGACACTTACCCCAAGGACTGTGGACTTGACTGTCATCCTCATCGCAGCGGTG	2104	DЬ
2304	TCTCGGTGACACTTACCCCAAGGACTGTGGACTTGACTGTCATCCTCATCGCAGCGGT	2245	Qy
2103	AGCTTCTGGGTCAACATCTCTAACTGCAGCCCCACGAGCGGCAAGCAGCTAGACCTGCTC	2044	Db
2244	GCTTCTGGGTCAACATCTCTAACTGCAGCCCCACGAGCGGCAAGCAGCTAGACCTGCT	2185	Qy
2043	GCTGAGGAGATCTTCAGCCTGGACGAGGATGTGCTCCCCCAAGCCAAGCTTCCACCATCAC	1984	Db
2184	CTGAGGAGATCTTCAGCCTGGACGAGGATGTGCTCCCCCAAGCCAAGCTTCCACCATCA	2125	Qy
1983	AGCGGCGTGGTCTGCCAGACAGGGCGCGCATTCATGATCATCCAGGAGCAGCGGACCCGG	1924	Db
2124	GCGGCGTGGTCTGCCAGACAGGGCGCGCATTCATGATCATCCAGGAGCAGCGGACCCG	2065	Qy
1923	TCCTGGAACATCAGCGTGCCCAGAGACCAGGTGGCCTGCCT	1864	Db
2064	CCTGGAACATCAGCGTGCCCAGAGACCAGGTGGCCTGCCT	2005	Qy
1863		1804	Db
2004	CAA-GGTCTACCTGAGGACCCCCAACTGGGACCGGGGCCTGCCATCCCTCACCTCTGT	1946	Qy
1803	AGGAAGGCCGTTTTCACGGTGACCCCTGACACAAAA	1744	дb
1945	CCTTTATACCTTATTTCAAAGAGGAAGGCGTTTTCACGGTGACCCCTGACACAA	1888	Qy
1743		1684	da
1887	CGCA-CCTTTGCCCCCAGCTTCCA-ACAAGAGGCCTCCAGGCAGGGTCTGACG	1833	Qy
1683	CTGCCCGGGAGGCTCTATCAAAGCAGATCCAGGTGAAGCAGGAACATCTCGGGTGACCCC	1624	ДĎ
1832	TGCCCGGGAGGCTCTATC-AAGCAGATCCAGGTGAAGCA-GAACATCTC-GGTGACC	1776	Qy
1623	CAGCTTCAGCTACCTCGTGGCCAGTGCCATACCCAGCCAG	1564	Db
1775	AGCTTCAGCTACCTCGTGGCCAGTGCCATACCCAGCCAGGACCTGTACTTCGGCTCC	1716	Оу

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The polynucleotide sequences given in AAA26346 to AAA26458 encode the CC human secreted proteins given in AAY91451 to AAY91691. The human secreted CC proteins can have activities based on the tissues and cells they are CC expressed in Examples of the activities are: Cytostatic; antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic; cantialthma; antipsoriatic; and cardiant. The polynucleotides and their corresponding secreted proteins are useful for preventing, treating or cameliorating medical conditions, e.g. by protein or gene therapy. Also cc pathological conditions can be diagnosed by determining the amount of the polynucleotides. Specific uses are described for each of the cc polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cc cancer, tumours, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, diseases of the immune system, cc altergies, Alzheimer's and behavioural disorders, schizophrenia, cc ardiovascular disorders, reproductive disorders, schizophrenia, cc cardiovascular disorders, reproductive disorders, gastrointestinal cord disorders, respiratory disorders and metabolic disorders. The proteins care also useful for identifying their binding partners. Cc AAA26337 to AAA26345 and AAY91450 are sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disorders, immune disease
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Best Loc Matches Query Match Local Sir hes 2189; Similarity Conservative 508 A; 35.4%; 99.0%; 12; Score 2179; DI Pred. No. 0; 12; Mismatches BB 21; 7; Length Indels ω, Gaps

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CDNA sequence encoding for PR05773 polypeptide

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DT 44-C Human secretory and transmembrane; PRO; mammalian; cancer; lung, breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alcartilage; ear; proliferation; glucose; free fatty acid; skelet; adipocyte; A-peptide; factor VIIA; gene therapy; ss. skeletal muscle;

WO200140466-A2

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AAS21244-AAS21518 encode for novel human secretory and transmembrane CC PRO polypeptides. The PRO polypeptides are useful to detect other CC PRO polypeptides, to link bioactive molecules to cells expressing CC PRO polypeptides, to modulate biological activities of cells expressing CC PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. CC Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the cartilage, the proliferentiation of chondrocytes, the proliferation or CC gene expression in pericyte cells, the release of proteoglycans from CC artilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide CC factor VIIA. The PRO polypeptides can be used in assays to identify collecules involved in binding interactions. The polynocleotides encoding PRO polypeptides can be used in gene therapy.
                    Query Match
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Matches 1119;
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   TTCCAAGTTTTGGTCCAACATCCACAAAATGAAAGCAATAA
                                                                                                           ACCAACCCCGAGGTGTTCAAGCTGGAGGACAAGCAGCCTGGGAACATGGCGGGGAACTTC
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25-MAY-2000;
09-JUN-2000;
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, used for detecting presence of prostate cancer, stage of prostate cancer
                                                                                                                                                                                                                                                                             Sequence 1031
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13-DEC-2000;
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pharmacogenomic marker; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                 selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastatized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cer in a patient;
assessing the efficacy of a therapy
CTTTTTCTTTTTTTTTAATGTGAGACAGGATCTCATTCTGTTGCCTAGGCTGGAGTGC
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                                                                                99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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        RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detection; diagnosis; antisense therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (5'-primer)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes primer sets for synthesising 5602 CC full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of CC the 5602 nucleotide sequences defined in the specification, where the CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the CC complementary strand of a polynucleotide which comprises a 5'-end sequence complementary to a CC polynucleotide which comprises a 3'-end sequence complementary to a CC polynucleotide comprises a 3'-end sequence, where the CC the 5'-end sequence?'3'-end sequence is selected from those defined in CC the 5'-end sequence?'3'-end sequence is selected from those defined in CC the 5'-end sequence?'3'-end sequence is selected from those defined in CC the specification. The primer sets can be used in antisense therapy and CC in gene therapy. The primers are useful for synthesising polynucleotides, CC particularly full-length cDNAs. The primers are also useful for the particularly full-length cDNAs. The primers allow obtaining of the full-length CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and CC AAH35631 to AAH13742 represent human cDNA sequences; and AAH13629 to AAH13622 cof the present oligonucleotides, all of which are used in the exemplification cof of the present invention.
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Best Local S
Matches 654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 659
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TACACCTCCCATGGTTCCACCCCAGAAATGTCTCCGGCTTCAGCATTGCAAACCGCTCAT
                                                          CCTTCTGCAGCAATGGCACTGTGTCCCGGATCAAGATGCAAGAAGAAGGAGTGAAAATGGCCT
                                                                                                                                                                                                                                                             CAGACGGAGTCACTCCACTCCATCAGCGGCGAATCGATGCCACCGTGGTCAGGATCGGAA
                                                                                                                                                                                                                                                                                                                        GTTTAGAGCTGCAGTTTTCCATCCCTCGCCTGAGGCAGATCGGTCCGGGTGAGAGCTGCC
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                                                                                                                                                                                                                                            CAGACGGAGTCACTCCCATCAGCGGCCGAATCGATGCCACCGTGGTCAGGATCGGAA
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3, Sugiyama
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T, Wakama
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Wakamatsu
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Pred. No. 5.4e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G; 151
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C, Otsuki
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RESULT 9
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portions of proteins which are associated with human colon tumours.

The invention also specifically discloses 8 human colon tumour proteins (AAB11897-B11904). The nucleic acids, the polypeptides they encode, and antigen presenting cells (APCs, preferably dendritic cells) expressing such polypeptides may be used in vaccines that target tumour cells, especially colon tumour cells, thereby inhibiting the development of cancer. T-cells specific for the polypeptide expressed by the APC are used to remove tumour cells from biological samples, especially blood or fractions thereof. The sample or the isolated T-cells specific for the polypeptide can then be used to inhibit cancer development. CD4 + and/or CD8+ T-cells from a patient may be incubated with a polypeptide or nucleic acid of the invention, or an APC expressing such a polypeptide, to cause the proliferation of specific T-cells. The T-cells can be cloned and then administered back to the patient to inhibit cancer
                                                                                                                                                                                                                                                                                                                                                                                           23-DEC-1998;
02-JUL-1999;
22-SEP-1999;
19-NOV-1999;
02-DEC-1999;
                                                                                                                                                                                                                                                                                                                         Xu J,
Wang
                                                                                                                                                                                                                                            New colon tumor polypeptides especially colon cancer, and progression of the cancer -
                                                                                                                                                                                                                                                                                                  WPI;
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                                                                                                                                                                                          Sequences AAA77722-A78199 represent 478 cDNAs encoding proteins
                                                                                                                                                                                                                    Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human colon tumour polypeptide; tumour antigen; cancer; vaccine;
immunotherapy; diagnosis; progression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA encoding
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                                                                                                                                                                                                                   1; Page 196; 229pp; English.
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Muqiu J;
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99US-0347496.
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99US-0454150.
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RESULT 10
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Best Loc
Matches
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                                                                                                                                                                                                                                                      3608
                                                                        Human;
                                                                                              Colon tumour
                                                                                                                                                                    AAI28813 standard; cDNA;
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                                                                                                                    12-OCT-2001
                                                                                                                                             AAI28813;
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                                                          immunogenic;
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Local Similarity
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                                                                     immunotherapy; diagnosis; colon cancer; colon tumour;
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                                                         gene
                                                                                              related
                                                                                                                   (first entry)
                                                          therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.8%;
                                                                                            determined cDNA sequence for clone 25928
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                                                          vaccine;
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Pred. No. 2.8
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                                                          cancer;
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                                             CC associated with inappropriate colon tumour associated protein (TCAP)
CC expression, such as colonic cancer. For example, (I) and (II) may be
CC used to treat disorders associated with decreased expression by
CC rectifying mutations or deletions in a patient's genome that affect the
CC activity of TCAPs by expressing inactive proteins or to supplement the
CC produce the TCAP proteins, by inserting the nucleic acids into a host
CC complementary sequences may also be used as DNA probes in diagnostic
CC complementary sequences may also be used as DNA probes in diagnostic
CC quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. (I) may
CC and in assays to identify modulators of TCAP expression and activity.
CC Anti-(I) antibodies and antagonists may also be used to down regulate
CC (e.g. by enzyme linked immunosorbant assay (ELISA)). AA128460 to AAN29512
CC and AAM24494 to AAM24523 represent nucleotide and amino acid sequences
CC given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-FEB-2000;
06-MAR-2000;
19-MAY-2000;
29-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the polynucleotides (II) that encode them. (I) have cytostatic activity. (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prevention,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-441847/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ž
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10-JAN-2000;
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વ GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present invention describes colon tumour associated proteins (I) and polynucleotides (II) that encode them (IV have noterial)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumor associated proteins and nucleic acids useful ntion, diagnosis and treatment of colonic cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2:
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E, Wang T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page
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2000US-0480321.
2000US-0504629.
2000US-0519444.
2000US-0575251.
2000US-0609448.
2000US-0649811.
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Sequence 544 BP; 138 A; 123 C; 113 G; 170 T; 0 other;

Query Match Best Local :

99.8%;

Score 542.4; DB 22 Pred. No. 2.8e-111;

DB 22;

Length 544;

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Matches
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                                    3248
                                                                                                                                             3068 CCTGAGTCACCTAGCATAGGGTTGCAGCAAGCCCTGGATTCAGAGTGTTAAACAGAGGCT
                  181
                                                      121
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                                                                                                                                                               Local Similarity
les 543; Conserv
                                                                                                                           CTCATACTAACTGGTTTGGATGCCTGGGTTGTGACTTCTACTGACCGCTAGATAAACGTG
                                                                                                          TGCCCTCTTCAGGACAACAGTTCCAATTCCAAGGAGCCTACCTGAGGTCCCTACTCTCAC
                                                                                                                                                               Conservative
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RESULT 11
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ID AAS58659;
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AC AAS58659;
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AC AAS58659;
XX
DT 13-FEB-2002 (first entry)
DT 13-FEB-2002 (first entry)
DT 13-FEB-2002 (first entry)
DE CDNA #1335 encoding portion
KW Human; colon tumour protein
CS Homo sapiens.
XX
PN W0200173027-A2.
XX
PN WPI; 2001-611627/70.
X
                                                         Th present invention relates to the isolation of novel cDNA sequences encoding for at least an immunogenic portion of human colon tumour proteins. The sequences of the invention are useful in pharmaceutical compositions and vaccines for the prevention and treatment of cancers such as colon cancer. They are also useful for the diagnosis and monitoring of such cancers. Antibodies to the colon tumour proteins and antigen presenting cells that express polynucleotides encoding colon tumour proteins can be used to inhibit the development of cancers. T-cells that react specifically with colon tumour proteins are useful for removing tumour cells from samples (e.g. blood) and for cancer treatment. The polynucleotides sequences are also useful ir gene therapy. AAS57325-AAS5880 represent the cDNA sequences of the invention that encode for portions of human colon tumour proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 266; 299pp; English.
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04-MAY-2000; 2000US-202024P
05-MAY-2000; 2000US-202189P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New colon tumour proteins and related nucleic acid, useful treatment, prevention, diagnosis and monitoring of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3548
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RESULT 12
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ID AAS577
XX AAS577
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XX DI 13-FEI
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Best Local :
                                                                                      24-MAR-2000; 2000US-191597P.
04-MAY-2000; 2000US-202024P.
05-MAY-2000; 2000US-202189P.
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                                                                                                                                                                                                                                                                       WO200173027-A2
                                                                                                                                                                                                                                                                                                                                                             Human;
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  Meagher MJ,
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                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                             therapy; cytostatic;
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Best Local S
Matches 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and antigen presenting cells that express polynucleotides encoding colon tumour proteins can be used to inhibit the development of cancers. T-cells that react specifically with colon tumour proteins are useful for removing tumour cells from samples (e.g. blood) and for cancer treatment. The polynucleotides sequences are also useful gene therapy. AAS57325-AAS58880 represent the cDNA sequences of the invention that encode for portions of human colon tumour proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encoding for at least an immunogenic portion of human colon tumour proteins. The sequences of the invention are useful in pharmaceutical compositions and vaccines for the prevention and treatment of cancers such as colon cancer. They are also useful for the diagnosis and monitoring of such cancers. Antibodies to the colon tumour proteins
                                                                                                                                                                                                                                                                                                                                                                               3308
             AAH13321 standard; cDNA;
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es 536; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       colon tumour proteins and related nucleic acid, useful for atment, prevention, diagnosis and monitoring of cancer -
                                                                                                                                                                                                                                          TGCCTGTCCCCCAGGTGGTGGGAATAATTTACAATCTGTCCAACCAGAAAAGAATGTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTGAGTCACCTAGCATAGGGTTGCAGCAAGCCCTGGATTCAGAGTGTTAAACAGAGGCT
                                                                               ATTTA 544
                                                                                                       ATTTA 3612
                                                                                                                                   ATAAGANAAATTTCCTCAAGTTT-CATGTGCGGTTTTCCTAANTGCANNAATCCTTTGAC
                                                                                                                                                            ATAAGAGAAATTTCCTCAAGTTTCCATGTGCGGTTCTCCTAGCTGCAGCAATACTTTGAC
                                                                                                                                                                                                                 GTTCGTGGTTATCCCATTGTGGAAATTCATCTTGAATCCCATTGTCCTATAGTCCTAGCA
                                                                                                                                                                                                                                                                                                 TGCCTGTCCCCCAGGTGGTGGGAATAATTTACAATCTGTCCAACCAGAAAAGAATGTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to the isolation
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98.3%;
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Pred. No. 7.8e
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/.8e-107;
hes 8;
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5581 TCAGGGTCACTGGAAACAGTGAAGTGCCATTTGTTGAAGCCTACTGCATGCCAGCCCACT

TCAGGGCCCCTGAAACCAGTAAAGT-CCNTTTGTTAAACCTTCTGCAATGCCAGCCCACT

GCTCATCCACGTGGTCTGCCATGCCTACGAGGAAGGCCAGCGCATGCAGGACTGGTCTCT GNTCATCCACGTGGTTTTCCATGCCTTCGAGGAA-GCCAGCGCATGCAGGACTGGTCTCT

5700

Query Match Best Local Sim Matches 541;

Similarity

8.3%;

Conservative

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Pred. No. 6.60 0; Mismatches Score 509.4; Pred. No. 6.

.6e-104; nes 20; DB 22;

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Gaps

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The present invention describes primer sets for synthesising 5602 cc full-length cDNAs defined in the specification. Where a primer set cc comprises: (a) an oligo-dr primer and an oligonucleotide complementary strand of a polynucleotide which comprises one of cc the 5602 nucleotide sequences defined in the specification, where the cc oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises as sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end cc polynucleotide which comprises a 5'-end cc polynucleotide which comprises a 3'-end sequence complementary to a complementary and complementary complementary and complementary. The primers selected from those defined in the specification and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and camplementary without any specialised methods. AAH03166 to AAH13628 and complementary and complementary and complementary conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ota T,
Ishii
  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; SEQ ID 10156; 2537pp +
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27-AUG-1999;
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Sugiyama
  561 BP;
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; 2000JP-0183767.
; 2000JP-0241899.
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161 A; 136
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T, Wakama
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C; 120 G; 140 T; 4 other;
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Otsuki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; gene expression product; diagnosis; tumour; colon cancer colorectal adenocarcinoma; cell line SM480; cell proliferation; cytostatic; sarcoma; breast cancer; neoplasia; dysplasia; hyperplasia; ds.
                                                                                       Novel nucleic acids, used to develop products treatment of disorders involving unwanted cell particularly cancers, especially colon cancer
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Carroll E,
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                                              Claim 15; Page 280;
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Catino TJ, Derti A, Ford
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                                              469pp; English.
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                                                                                                   for the diagnosis proliferation,
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AAZ79917 to AAZ80766 represent double

stranded

cDNA clones

RESULT 1:
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DT 13-1
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13-FEB-2002

(first

entry)

AAS64483 standard; cDNA; 487

ВP

DNA encoding

novel human diagnostic protein

Human; chromosome mapping; gene mapping; gene therapy; forensic food supplement; medical imaging; diagnostic; genetic disorder;

forensic;

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the human colorectal adenocarcinoma (colon cancer) cell line SW480. The cDNA clones can be used to generate antisense oligonucleotides which can be used for antisense therapy. Methods and products from the present invention can be used for identifying and/or classifying cancerous cells present in a human tumour, particularly in solid tumours, e.g. carcinomas and sarcomas, e.g. breast or colon cancers. The cDNA clones can be used for developing agents for the diagnosis and treatment of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 636 BP; 155 A; 144 C;
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                GCATTTTATTCATTTCCTGTGCTTTAAATAAACAAATGT 5903
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xal Similarity 90.3%;
577; Conservation
                                                                                           TGTGTGGATCTGCAGTGCTTCACTGGAAATAATTTATTCATTGCAGATACTTTTTAGGTG
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                                                            TGTGTGGATCTGCAGTGCTTCACTGGAAATAATTTATTCATTGCAGATACTTTTTAGGTG
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smatches 54;
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                                                                                                                                                                                                                                                                                                                                                            CC polypertide (II) sequences. (I) is useful as hybridisation probes, complymerase chain reaction (PCR) primers, oligomers, and for chromosome cand gene mapping, and in recombinant production of (II). The polypucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques compared to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as food supplement. (II) and its binding partners are useful in medical comparing of sites expressing (II). (I) and (II) are useful for treating the compared of the polypeptide and polynucleotide expression or biological activity. The polypeptide and polynucleotide sequences have applications in constitutions for diagnostics, forensics, gene mapping, identification of mutations cand to produce other types of data and products dependent on DNA and cand to produce other types of data and products dependent on DNA and cand of the sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed cant for the pipe, intronibilities and not printed on the pipe.
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                                                                                                                                                                                                                                                                                                                                                           Sequence 487 BP; 131 A; 145 C; 120 G; 91 T; 0 other;
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23-AUG-2000;
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GGCAGCCAAAAAAGTTTCAGAAAGGGCGAAAGGACAATGACTCCCATGTGTATGCAGTCA
                                                                                                                                                                                            AGACAAACAAGGGCCCCGCTGTGGGTATCTACAATGGCAACATCAATACTGAGATGCCGA
                             AGACAAACAAGGGCCCCGCTGTGGGTATCTACAATGGCAACATCAATACTGAGATGCCGA
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)B; ABG00296.
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Similarity 100.0%;
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2000US-0649167.
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Pred. No. 8.3e-98;
0; Mismatches 0;
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                                                                                                                                                                              CCACCATATGCTCCAGGGCCCCAACTGCAAAGTTGGCCACTGAGGAGCCACCTCCTCGCT 2671
                                                    GCAGCAAGGACACAGTTCCCTTACTGAACACTCAGGAGCCCATGGAGCCAGCAGAAT
                                                                                                           CCCCTCCTGAGTCTGAGAGTGAACCGTACACCTTCTCCCATCCCAACAATGGGGATGTAA
                                                                                                                                                                CCACCATATGCTCCAGGGCCCCAACTGCAAAGTTGGCCACTGAGGAGCCACCTCCTCGCT
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Search completed: November Job time : 1161 secs 2002,

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Result
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Listing first 45 summaries
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1 MAGLNCGVSIALLGVLLLGA.....SSKDTDIPLLNTQEPMEPAE 836
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/Aa199, DAT:
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
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AAB12113	AAB12029	AAB48461	ABB91468	AAG68303	AAG68311	AAM78991	AAB85060	AAM40888	ABB57361	ABG04010	AAM39102	ABB12455	AAY57091	AAR98454	AAY56029	ABB70548	AAE23674	ABB06022	ABB59065	AAW67738	ABB91371	AAR92100	ABB71111	AAU38959	ABB64637	ABG28277	ABG23416	ABB06023	AAB42916	AAE20788	ABG65509	~1	70	AAM90342
	ter	g	Herbicidally activ	Human semaphorin G	Human semaphorin G	Human protein SEQ	Human serine prote	Human polypeptide	Œ				Human oligodendroc	Oligodendrocyte-my	Human BRCA2 tumour	sophila mel	rotein.	Human cubulin prot	sophila mei	Pig p105 zona pell	ally a	Human RIZ allele D			phila ı	l human	human	cubu	an	3b/c4	albu	an secreted pr	ubilin p	Human immune/haema

## ALIGNMENTS

RESULT 1

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AAM49641
ID AAM
Tumour-associated antigen; human; B345; cytostatic; cell communication; cell interaction; signal transduction; metastasis; cancer; colon; immunotherapy; carcinoma; lung; diagnosis.
                   WPI; 2002-171704/22.
N-PSDB; ABA99507.
                                                   Schweifer N,
                                                                                             07-JUL-2000; 2000DE-1033080.
19-APR-2001; 2001DE-1019294.
                                                                                                                               05-JUL-2001; 2001WO-EP07705
                                                                                                                                                    17-JAN-2002.
                                                                                                                                                                         WO200204508-A1
                                                                                                                                                                                                                                                              Human tumour-associated antigen B345 protein SEQ ID NO
                                                                                                                                                                                                                                                                                   17-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                         AAM49641;
                                                                                                                                                                                                                                                                                                                               AAM49641 standard; Protein; 836 AA
                                                                                                                                                                                               Homo sapiens.
                                                                        (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
                                                    Scherl-Mostageer M,
                                                    Sommergruber W,
                                                   Abseher R;
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New tumor-associated antigen B345, useful for diagnosis and

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Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel tumour-associated antigen, designated B345 which has cytostatic activity. B345 is involved in communication, interaction and/or signal transduction with extracellular components and ligands, especially in the metastatic potential of cancers, particularly of the colon. B345 or its immunogenic fragments, also the DNA that encodes it, are useful for immunotherapy of cancer, particularly carcinoma of lung or colon. Antibodies raised against B345 are useful for treatment and diagnosis of cancers that are associated with B345 expression, including their use for targeted delivery of cytotoxic or radioactive agents. Probes derived from B345 can be used to detect tumour-specific modulators. This sequence, and can be used to screen for B345 specific modulators. This sequence represents a human B345 tumour-associated antigen described in the invention.
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                                                      PRTVDLTVILIAAVGGGVLLLSALGLIICCVKKKKKTNKGPAVGIYNGNINTEMPRQPK
                                                                                                             SYLVASAIPSQDLYFGSFCPGGSIKQIQVKQNISVTLRTFAPSFQQEASRQGLTVSFIPY
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                                                                                                                                                                                                                                                                                                                                                                                                                     PRPVKQSRKFVPGCFVCLESRTCSSNLTLTSGSKHKISFLCDDLTRLWMNVEKTISCTDH
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRPVKQSRKFVPGCFVCLESRTCSSNLTLTSGSKHKISFLCDDLTRLWMNVEKTISCTDH
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                                     PRTYDLTVILIAAVGGGVLLLSALGLIICCVKKKKKTNKGPAVGIYNGNINTEMPRQPK
                                                                                                                                                                                                                                                                                                                                             RYCQRKSYSLQVPSDILHLPVELHDFSWKLLVPKDRLSLVLVPAQKLQQHTHEKPCNTSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QPGNMAGNFNLSLQGCDQDAQSPGILRLQFQVLVQHPQNESNKIYVVDLSNERAMSLTIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTVSRIKMQEGVKMALHLPWFHPRNVSGFSIANRSSIKRLCIIESVFEGEGSATLMSANY
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Pred. No. 0;
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                                              immunosuppressive; antiHIV; antiHiflammatory; nootropic; neuroprotective; antiallergic; osteopathic; antiArthritic; antibacterial; antidiabetic; antiasthma; antipsoriatic; and cardiant. The polynucleotides and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions on be diagnosed by determining the amount of the proteins in a sample or by determining the presence of mutations in the polynucleotides. Specific uses are described for each of the polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, diseases of the immune system, autoimmune diseases, hepatic and renal disease, schizophrenia, anticities and behavioural disorders, schizophrenia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUL-1998;
05-AUG-1998;
06-AUG-1998;
06-AUG-1998;
12-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                            The polynucleotide sequences given in AAA26346 to AAA26458 encode human secreted proteins given in AAY91451 to AAY91691. The human s proteins can have activities based on the tissues and cells they a expressed in Examples of the activities are: cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; secreted protein; diagnosis; cytostatic; immunosuppressive; antiHIV; antiinflammatory; nootropic; neuroprotective; antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic; antiasthma;
                                osteoporosis, arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated human
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DB; AAA26351.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ed human genes and the secreted polypeptides they diagnosis and treatment of e.g. cancers, neurologimmune diseases, inflammation or blood disorders
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Wei
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Y, Ni J, Florence
ess GA, Ebner R, (
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                              infections, AIDS, spinal
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 Tumour-associated antigen;
                      Human tumour-associated antigen
                                                                                          AAM49640
                                             17-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel tumour-associated antigen, designated B345 which has cytostatic activity. B345 is involved in communication, interaction and/or signal transduction with extracellular components and ligands, especially in the metastatic potential of cancers, particularly of the colon. B345 or its immunogenic fragments, also the DNA that encodes it, are useful for immunotherapy of cancer, particularly carcinoma of lung or colon. Antibodies raised against B345 are useful for treatment and diagnosis of cancers that are associated with B345 expression, including their use for targeted delivery of cytotoxic or radioactive agents. Probes derived from B345 can be used to detect tumour-specific modulators. This sequence, and can be used to screen for B345 specific modulators. This sequence represents a human B345 tumour-associated antigen described in the invention.
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19-APR-2001;
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immunotherapy; carcinoma; lung; diagnosis.
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                                       SRKFVPGCFVCLESRTCSSNLTLTSGSKHKISFLCDDLTRLWMNVEKTISCTDHRYCQRK
                                                    SRKFVPGCFVCLESRTCSSNLTLTSGSKHKISFLCDDLTRLWMNVEKTISCTDHRYCQRK
                                                                                              GNFNLSLQGCDQDAQSPGILRLQFQVLVQHPQNESNKIYVVDLSNERAMSLTIEPRPVKQ
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nilarity 90.3%;
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                            The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary of a polynucleotide which comprises one of
                                                                                                                                                                                                                                                                Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                    Claim
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the complementary strand of a polynucleotide which comprises one of 1502 nucleotide sequences defined in the specification, where the Appendix completes at least 15 nucleotides; or (b) a combination of the complementary to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TVILIAAVGGGVLLLSALGLIICCVKKKKKTNKGPAVGIYNGNINTEMPRQPKKFQKGR
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Sugiyama T, Wakama
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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A, Nagai K,
                                                                                                                                                                                                               English.
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(, Otsuki
  or (b) a combination mentary to the
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Best Local S
Matches 646
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les 646; Conservative
LATEEPPPRSPPESESEPYTFSHPNNGDVSSKDTDIPLLNTQEPMEPAE
                                                                                   DNDSHYYAVIEDTMYYGHLLQDSSGSFLQPEVDTYRPFQGTMGVCPPSPPTICSRAPTAK
                                                                                                                                                          VILIAAVGGGVLLLSALGLIICCVKKKKKKTNKGPAVGIYNGNINTEMPRQPKKFQKGRK
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                                LATEEPPPRSPPESESEPYTFSHPNNGDVSSKDTDIPLLNTQEPMEPAE 836
                                                                                                                                      VILIAAVGGGVLLLSALGLIICCVKKKKKKTNKGPAVGIYNGNINTEMPRQPKKFQKGRK
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                                                                                                                                                                                                                             IQEQRTRAEEIFSLDEDVLPKPSFHHHSFWVNISNCSPTSGKQLDLLFSVTLTPRTVDLT
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                                                                   DNDSHVYAVIEDTMVYGHLLQDSSGSFLQPEVDTYRPFQGTMGVCPPSPPTICSRAPTAK
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Pred. No. 1.7e-288;
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29-JUN-2000

(first

entry)

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The polynucleotide sequences given in AAA26458 encode the C. human secreted proteins given in AAA2451 to AAA26458. The human secreted proteins given in AAA29451 to AAA26459. The human secreted contains can have activities based on the tissues and cells they are expressed in Examples of the activities are: cytostatic; antiallargic; osteopathic; antiarthrith; antibacterial; antidiabetic; antialsthma; antipsoriatic; and cardiant. The polynucleotides and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also compations in a sample or by determining the presence of mutations in the polynucleotides. Specific uses are described for each of the polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, diseases of the immune system, allergies, Alzheimer's and behavioural disorders, schizophrenia, cardiovascular disorders, reproductive disorders, schizophrenia, cardiovascular disorders, reproductive disorders, gastrointestinal cord clasorders, respiratory disorders, spinal cord injuries, transplant rejection, diabetes, asthma, sepsis, acne, psoriasis, can also be used as food additives or preservatives. The proteins are also useful for identifying their binding partners. Capacition of the preservatives. Capacition of the preservatives.
                    S
                                                   Matches
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Best Local
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06-AUG-1998;
12-AUG-1998;
                                                                                                                    Sequence
                                                                                                                                                   exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 18; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated human genes and the secreted polypeptides they encode, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
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osteopathic; antiarthritic; antibacterial; antidiabetic; antiasthma;
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antiHIV; antiin
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Lafleur D, Wei Y,
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05-AUG-1998;
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1 MAGLNCGVSIALLGVLLLGAARLPRGAEAFEIALPRESNITVLIKLGTPTLLAKPCYIVI 60
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                                                                   Similarity
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98US-0095486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cardiant; gene therapy; cancer; neurological disorder;
inflammation; blood disorder; tumour.
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                                                                                                                                                the present invention.
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                                                                 49.0%;
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Florence KA, Young PE,
                                                 0
                                                 Score 2155; DB 21;
Pred. No. 4.1e-179;
0; Mismatches 0;
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E, Brewer
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RESULT 6
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18-FEB
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17-MAY
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                                                                                                                                                                                                                                                                                               breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpl cartilage; ear; proliferation; glucose; free fatty acid; skeletal adipocyte; A-peptide; factor VIIA; gene therapy.
                                                                                 18-FEB
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                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTVSRIKMQEGVKMALHLPWFHPRNVSGFSIANRSSIKRLCIIESVFEGEGSATLMSANY
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                                                                                                                                                                                                                                                                                                                                            PRO5773 polypeptide sequence
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-1999;
-1999;
     99WO-US28301.
99WO-US28551.
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99WO-US28555.
99WO-US3099.
99WO-US3099.
99WO-US3099.
99WO-US3099.
2000WO-US0376.
2000WO-US0376.
2000WO-US04214.
2000WO-US04214.
2000WO-US04214.
2000WO-US04565.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANUI2172-ANUI2446 represent novel human secretory and transmembrane CC PRO polypeptides. The PRO polypeptides are useful to detect other CC PRO polypeptides, to link bloactive molecules to cells expressing CC PRO polypeptides, to modulate biological activities of cells expressing CC PRO polypeptides, and to detect the presence of mammalian lung, colon, CC breast, prostate, recttal, cervical or liver tumours by comparing PRO CC polypeptide expression in a cell sample to that in a control sample. CC some of the 275 sequences are also useful to stimulate the release of cumour necrosis factor-alpha (TNF-alpha) from human blood, the CC proliferation or differentiation of chondrocytes, the proliferation or CC gene expression in pericyte cells, the release of proteoglycans from CC artilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by Skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide CC molecules involved in binding interactions. The polynucleotides encoding CC PRO polypeptides can be used to generate probes, antisense RNA/DNA, CC transgenic or knock out animals and can be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                           Matches
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30-MAY-2000;
02-JUN-2000;
10-NOV-2000;
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Smith V, Ste
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                                                                                                                                                                                                                                                                                                                        lated, secretory and transmembrane PRO polypeptide used to detect er PRO polypeptides, link bloactive molecules to cells expressing polypeptides, and detect the presence of mammalian tumours e.g. y, breast, prostate, cervical
                QPGNMAGNFNLSLQGCDQDAQSPGILRLQFQVLVQHPQNESNK
                                                                                                                                                                                                           LNRTFIWDVKAHKSIGLELQFSIPRLRQIGPGESCPDGVTHSISGRIDATVVRIGTFCSN
                                                          PEGFPEDELMTWQFVVPAHLRASVSFLNFNLSNCERKEERVEYYIPGSTTNPEVFKLEDK
                                                                                                                                              GTVSRIKMQEGVKMALHLPWFHPRNVSGFSIANRSSIKRLCIIESVFEGEGSATLMSANY
                                                                                                                             GTVSRIKMQEGVKMALHLPWFHPRNVSGFSIANRSSIKRLCIIESVFEGEGSATLMSANY
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QPGNMAGNFNLSLQGCDQDAQSPGILRLQFQVLVQHPQNESSE 343
                                                                                                                                                                                             LNRTFIWDVKAHKSIGLELQFSIPRLRQIGPGESCPDGVTHSISGRIDATVVRIGTFCSN
                                                                                                                                                                                                                                                           SKRHITMLSIKSGERIVFTFSCQSPENHFVIEIQKNIDCMSGPCPFGEVQLQPSTSLLPT
                                                                                                                                                                                                                                                                                                                                                                                         Similarity 99.4
41; Conservative
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ME, Goddard A, God
ME, Tumas D
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2000WO-US14941.
2000WO-US15264.
2000WO-US30873.
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A, Godowski PJ, Gurney AL, Sh
Tumas D, Watanabe CK, Wood WI,
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Pred. No. 1.8e
2; Mismatches
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1.8e-146;
nes 0;
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RESULT 7
AAY91593
                                              The polynucleotide sequences given in AAA26458 encode the CC proteins can have activities based on the tissues and cells they are CC proteins can have activities based on the tissues and cells they are CC expressed in Examples of the activities are: cytostatic; antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic; cantiasthma; antipsoriatic; and cardiant. The polynucleotides and their corresponding secreted proteins are useful for preventing, treating or cameliorating medical conditions, e.g. by protein or gene therapy. Also cc pathological conditions, e.g. by protein or gene therapy. Also cc pathological conditions, e.g. by protein or gene therapy. Also cc pathological conditions can be diagnosed by determining the amount of the polynucleotides. Specific uses are described for each of the cc polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cc cancer, tumours, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, developmental abnormalities can feetal deficiencies, blood disorders, developmental abnormalities consteoporosis, arithritis, infections, AlDS, spinal cord injuries, cc ardiovascular disorders, reproductive disorders, schizophrenia, cc cardiovascular disorders, reproductive disorders, gastrointestinal cd disorders, respiratory disorders and metabolic disorders. The proteins craft in proteins are also useful for identifying their binding partners.

CC AAA26337 to AAA26345 and AAY91450 are sequences used in the
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05-AUG-1998;
06-AUG-1998;
06-AUG-1998;
12-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; secreted protein; diagnosis; cytostatic; immunosuppressive; antiHTV; antiinflammatory; nootropic; neuroprotective; antiallergic; osteopathic; antiarthritic; antibacterial; antidabetic; antiasthma; antipsoriatic; cardiant; gene therapy; cancer; neurological disorder; immune disease; inflammation; blood disorder; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated human genes and the secreted polypeptides they encode, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 18; 634pp; English.
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Lafleur D,
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                                  to AAA26345 an 
lcation of the
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Wei Y,
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Wei Y, Ni J, Florence KA,
Endress GA, Ebner R, Olse
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98US-0095486.
98US-0095454.
98US-0095455.
98US-0096319.
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PE, Brewer
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RESULT 8
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                                                                       CC polypeptide (II) sequences. (I) is useful as hybridisation probes, colypnerase chain reaction (PCR) primers, oligomers, and for chromosome cc and gene mapping, and in recombinant production of (II). The cc and gene mapping, and in recombinant production of (II). The cc and gene mapping, and in recombinant production of (II). The cc and gene mapping, and in recombinant production of (II). The cc and activity of (II) is useful in gene therapy techniques cc (II). (II) is useful for generating antibodies against it, detecting or cc quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical cc imaging of sites expressing (II). (I) and (II) are useful for treating cc disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in creating creations for genetic disorders or other traits to assess biodiversity and creating creating and creating contract dependent or now and and creating contract dependent or now and and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnostics, forensics, responsible for genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
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23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
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                            to produce other types of data and products dependent on DNA no acid sequences. ABG00010-ABG30377 represent novel human
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17-JUL-2000; 2
03-AUG-2000; 2
15-SEP-2000;
                The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; tomato; monkey; dog; sea urchin; expressed sequence tag; ES; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.
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                                                                                                      Claim
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Drmanac RA,
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24-FEB-2000;
16-MAY-2000;
17-MAY-2000;
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Wright RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; purified secretory polypeptide; cell proliferative disorder; cancer; immune system disorder; neurological disorder; mental disorder; motor neuron disorder; demyelinating disorder; neuromuscular disorder; central nervous system disorder; enzyme linked immunosorbent assay; ELISA; gene therapy.
         Sequences AAU69432-AAU69511 represent purified secretory polypeptides of the invention. The polypeptides and their associated polynucleotides can be used in the treatment, prevention and diagnosis of diseases associated the inappropriate secretory protein expression. These diseases include reliferative disorders such as atherosclerosis and psoriasis,
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                                                                                                                                                                            Bratcher SR,
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TC, Daniels SE;
LB, Hillman JL,
Stockdreher TK,
system disorders
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RESULT 11
AAM90342
ID AAM90
XX AAM90
AC AAM90
XX U7-NC
XX Human
XX Cytos
XX O9-AU
XX O9-AU
XX HOMO
PN WO200
PR 31-JA
PR 11-JA
PR 16-MA
PR 16-MA
PR 11-MA
PR 11-MA
PR 11-MA
PR 11-MA
PR 30-JU
PR 07-JU
PR 07-JU
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PR 11-JU
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Best Local
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                                                  28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
                                                                                                                                       18-APR-2000;
19-MAY-2000;
07-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neurofibromatosis and neuromuscular disorders such as cerebral palsy and muscular dystrophy. Target polynucleotides in a sample can be detected by hybridising the sample with a probe sequence complementary to the target polynucleotide, under conditions in which a hybridisation complex is formed, and detecting the presence or absence of the complex. The polypeptides may also be used as antigens in the production of antibodies against secretory proteins and in assays to identify modulators of protein expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the sequences of the invention in samples e.g. by enzyme linked immunosorbent assay (ELISA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          asthma and diabetes mellitus, neurological disorders such as epilepsy an Parkinson's disease, mental disorders such as schizophrenia and seasonal affective disorder (SAD), motor neuron disorders such as amyotrophic lateral sclerosis, demyelinating disorders such as multiple sclerosis, central nervous system disorders such as mental retardation and
                                                                                                                                                                                                             02-MAR-2000;
16-MAR-2000;
                                                                                                                                                                                                                                                04-FEB-2000;
24-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANRSSIKRLCITESVFEGEGSATLMSANYPEGFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RKNIELYVRPMSLLGEVQLQPSTSLLPTLNRTFIWDVKAHKSIGLELQFSIPRMRQIGPV 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immune/haematopoietic antigen SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immune; haematopoietic; immune/haematopoietic antigen; cancer;
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                              2000US-0190076.

2000US-0198123.

2000US-0205515.

2000US-0209467.

2000US-021648.

2000US-021647.

2000US-0216487.

2000US-0217487.

2000US-0217487.
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2000US-0184664
                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapy; vaccine; metastasis
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Pred. No. 2.6e-37;
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2000US-0220964

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05-DEC-2000
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17-NOV-2000
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17-NOV-2000;
17-NOV-2000;
AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially
                                                                                                                                                                                                               Nucleic acids encoding useful for preventing, metastasis -
                                                                                                                                                                                       Claim
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DB; AAK63123.
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2000US-0251988
2000US-0251868
2000US-0251868
2000US-0251868
2000US-0251889
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2000US-0251989
2000US-0251989
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2000US-0229343
2000US-0229344
2000US-0229509
2000US-0229513
2000US-0230438
2000US-0231242
2000US-0231244
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2000US-0232398
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14-AUG-2000 12-AUG-2000 22-AUG-2000 22-AUG-2000 22-AUG-2000 23-AUG-2000 23-AUG-2000 23-AUG-2000 25-SEP-2000 01-SEP-2000 01-SEP-2000

2000US-0227009. 2000US-0228924. 2000US-0229287.

2000US-0225214 2000US-0225266. 2000US-0225267. 2000US-0225268. 2000US-022527. 2000US-0225447. 2000US-0225757. 2000US-0225758. 2000US-0225758. 2000US-0225759. 2000US-0225759. 2000US-0226879. 2000US-0226879. 2000US-0226879.

114-SEP-2000 114-SEP-2000 21-SEP-2000 21-SEP-2000 25-SEP-2000 26-SEP-2000 27-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 20-OCT-2000 02-OCT-2000 03-OCT-2000 03-OCT-2000 04-OCT-2000 05-OCT-2000 06-OCT-2000 07-OCT-2000 07-OCT-2000 08-NOV-2000 08-NOV-2000 08-NOV-2000 08-NOV-2000

2000US-0233064
2000US-0234623
2000US-0234274
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2000US-0235484
2000US-0235484
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2000US-0237037
2000US-0237039

2000US-0241221 2000US-0241785 2000US-0241786 2000US-0241787 2000US-0241808 2000US-0241809 2000US-0241826 2000US-024617 2000US-024617 2000US-0246475

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RESULT 12
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Best Local :
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to AAK87694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer metastases of haematopoietic-derived cells. AAK64703 represent human immune/haematopoietic antigen genomic rom the present invention. AAK5492 to AAK54950 and AAM82169 equences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                        protein
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857
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711
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1551
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491
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                                                                                                                                                                                                                                                                                      "endoplasmatic import signal sequence"
                 "potential N-glycosylation
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"potential N-glycosylation
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                                                                                                  "potential N-glycosylation
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                                                                 N-glycosylation
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3533
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                                                                     TPRTVDLTVIL 670
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                    disorders (e.g. cancers and Gaucher's disease), ard orders (e.g. Scimitar syndrome, Chaga's cardiomypathy and coronary arteriosclerosis), angiogenic disorders (e.g. corneal graft neovascularisation and diabette retinopathy), neurological disorders (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), infectious diseases and/or for promoting wound healing, regeneration and/or chemotaxis. The nucleic acid molecules may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples. The polypeptides may also be used as antigens in the production of antibodies and in assays to detect and in assays to detect and quantitate they are not seed as antigens in the production of antibodies and in assays to detect and activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acids encoding the proteins and the proteins themselves may be used in the prevention, diagnosis and treatment of diseases including immune disorders (e.g. multiple sclerosis, systemic lupus erythematosus and human immunodeficiency virus (HIV) infections), hyperproliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; secreted protein; immunomodulatory; antisclerotic; dermatological; immunosuppressive; antiinflammatory; anti-fily; immunostimulant; cytostatic; cardiant; vascular; anti-angiogenic; ophthalmological; neuroprotectant; nootropic; anticonvulsant; vaccine; antialzheimers; antiparkinsonian; antimicrobial; vulnerary; gene therapy; immune disorder; hyperproliferative; cardiovascular; angiogenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 364-366; 380pp; English.
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                                                                      401 CDDLTRLWMNVEKTISCTDHRYCQRKSYSLQVPSDILH------LPV-----ELHDF
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                                                                                                                                                                                                                                                                                        225 SVFEGEGSATLMSANYPEGFPEDELMTWQFVVPAH---LRASVSFLNFNLSNCERKEERV
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                                                                                                          CTL------SIRDTRESDAGTYVFCVERGNMKWNYKYDQLSVN-VTAS
                                                                                                                                              NKIYVVDLSNERAMSLTIEPRPVKQSRKFVPGCFV-CLESRTCSSNLTLTSGSKHKISFL
                                                                                                                                                                                                                                                        TVQEGLCVSVLCSFSYPQN-----GWTASDPVHGYWFRAG-
                                  QDLLSRYRLEVPESVTV-----QEGLCVSVPCSVLYPHYNWTASSPVYGSWFKEGADI
                                                                                                                                                                                  SRNIPVATNNPARAVQEE--------TRDRFH-LLGDPQNKD
                                                                                                                                                                                                                  EYYIPGSTTNPEVFKLEDKQPGNMAGNFNLSLQGCDQDAQSPGILRLQFQVLVQHPQNES
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DB; AAF76851.
                                                                                                                                                                                                                                                                                                                                                 Similarity
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ч.уркdrlslvlvpaqklqqнтн--
                                                                                                                                                                                                                                                                                                                                                                                                        595 AA;
                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence is one of 18 novel human secreted proteins.
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                                                                                                                                                                                                                                                                                                                                                 Score 126;
Pred. No. 0.
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-EKPCNTSFSYLVASAIPSQDLYFGSF
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RESULT 14
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human serum albumin; HSA; cancer; reproductive disorder;
digestive disorder; immune disorder; endocrine disorder;
                                                                                                                                                                                                                                                                                                                                              cytostatic; antiinfertility; antiinflammatory; antiulcer;
immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;
neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
                         New fusion protein for treating disease e.g. diabetes comprises
                                                                                                                                           12-APR-2000; 2000US-229358P
25-APR-2000; 2000US-199384P
21-DEC-2000; 2000US-256931P
                                                                                                                                                                                                   12-APR-2001; 2001WO-US11988
                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                 osteopathic; antiarthritic.
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                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                              (HUMA-) HUMAN
                                                                                                                                                                                                                                                                                                                                                                                        haematopoietic disorder; neural disorder; connective
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                                                        2002-010886/01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VYAVIEDTMVYGHLLQDSSGSFLQPEVDTYRPFQGTMGVCPPSPPTICSRAPTAKLATEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GG----VLLLSALGLIICCVKKKKKKTNKGPAVGIYNGNINTEMPROPKKFOKGRKDNDSH
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Best Local Sin
Matches 135;
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                                                                                                                            GAGATALVFLYFCIIFVVVRSCRKKSAR-PAVGV--GDTGME-
                                                                                                                                                                                                  SNLGVLELPRVHVKDEGEFTCRAQN--PLGSQHISLSLQNEYTGKMRPISGVTLGAFG
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ARPQYPQEQEAIGYEYSEIN
                               PPPRSPPESESEPYTFSHPN 812
                                                                                              VYAVIEDTMVYGHLLQDSSGSFLQPEVDTYRPFQGTMGVCPPSPPTICSRAPTAKLATEE
                                                                                                                                                               GG---VLLLSALGLIICCVKKKKKKTNKGPAVGIYNGNINTEMPRQPKKFQKGRKDNDSH
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                                                                DANAVRG --
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                                                               ·SASQGPLIESPADDSPPHHAPPALATPSPEE - - GEIQYASLSFHK
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Pred. No. 0.085;
6; Mismatches 247;
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RESULT

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                                                                                                                                                                                                                                                                                                           The invention relates to a nucleic acid encoding a novel C3b/C4b complement receptor (CR)-like nucleic acid molecule. The C3b/C4b CR-like polypeptide and nucleic acid molecules may be used to treat, prevent, ameliorate, diagnose and/or detect diseases such as immune system disorders such as rheumatoid arthritis, psoriatic arthritis, inflammatory arthritis, osteoarthritis, inflammatory joint disease, autoimmune disease, multiple sclerosis, lupus, inflammatory bowel disease, transplant rejection, nervous system disorders (e.g. Alzheimer's disease), ischaemic conditions, metabolic disorders (e.g. obesity and disease), ischaemic conditions, metabolic disorders (e.g. obesity and disease) and infertility. The invention is useful in gene therapy. The present sequence is rat C3b/C4b complement receptor like protein.
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                                                      1225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid encoding a novel C3b/C4b Complement Receptor-like nucleic acid molecule, useful for treating, preventing and diagnosing rheumatoid arthritis, psoriatic arthritis, inflammatory arthritis, and multiple sclerosis
                                                                                                                                                                                                                                                                 Sequence
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5387 ACC	578 A-G	5330 AG	636	5270	ery Match	; ORGANISM: Homo sapiens ; FEATURE: ; NAME/KEY: misc_feature ; LOCARTION: (1)(636) ; OTHER INFORMATION: n = A,T,C or G US-09-328-111-370	FTWARE: D ID NO 3 ENGTH: 6	JRRENT FI	TLE OF I	PLICANT	PLICANT	PLICANT:	PLICANT PLICANT PLICANT	T 1 )-328-111  uence-37  ent No.		3 211 4 210 5 210	0 211	7 212 8 211 9 211	4 212 5 212 6 212	3 21	8 214 9 213 0 213
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ACCACGTGGCCATTTTCCTTC	CCCTTAAGGNNG	r AGGCTG	AAGCCCTTCCAAACAGG	AGCCCCTTC	3 4; Leng: 107; 54; Inde:		7			EXPRESSION											
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US-09-798-096-10/c
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Patent No. 6399378
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF
FILE REFERENCE: RTS-0207
                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID
SEQ ID NO 10
LENGTH: 99500
                                                                                                                                                                                                                                    Query Match
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CURRENT FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 89
                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo
     66002
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TCCCACCTCAGCCTCCCAAATAGCTGGGATCACTGGCACCAAACCACCATGCCCAGCTAA-
                                                                                                                  GGAGTGCAGTGGCGCAATCTCGGCTCACTGCAACCTCTGCCTCCTGGGCTCAAGCAATTC
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RESULT 4
US-08-481-968A-4/c
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                                                      GENERAL INFORMATION:
APPLICANT: Huber, Brian
APPLICANT: Richards, Cynthia
APPLICANT: Richards, Cynthia
TITLE OF INVENTION: Molecular Constructs Compr
TITLE OF INVENTION: Transcriptional Regulatory
FILE REFERENCE: PB1087US4
                                                                                                                                                                      Sequence 4, Application Patent No. 6300490
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Best Local Similarity 81.7%;
Matches 264; Conservative
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TITLE OF INVENTION: Antigen for Expression Targeting
FILE REFERENCE: PB1508USW
CURRENT APPLICATION NUMBER: US/08/646,301A
CURRENT FILING DATE: 1996-05-16
NUMBER OF SEQ ID NOS: 25
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SEQ ID NO 1
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CURRENT APPLICATION NUMBER: US/08/481,968A CURRENT FILING DATE: 1998-06-07 NUMBER OF SEQ ID NOS: 36
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ORGANISM: Homo
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                                                                                            Molecular Constructs Comprising a Carcinoembryonic
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Pred. No. 5.8e-42;
0; Mismatches 58;
                                                                             Region
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Sequence 4, Application US/08154712B
Patent No. 6337209
GENERAL INFORMATION:
APPLICANT: Huber, Brian
APPLICANT: Richards, Cynthia
TITLE OF INVENTION: Molecular Constructs Co.
TITLE OF INVENTION: Sequence
FILE REFERENCE: PB1087US3
CURRENT APPLICATION NUMBER: US/08/154,712B
CURRENT FILING DATE: 1993-11-19
NUMBER OF SEQ ID NOS: 36
SOFTMARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 11288
TYPE: DNA
ORGANISM: Homo sapiens
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US-08-154-712B-4/c
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Best Local Similarity 81.7%;
Matches 264; Conservative
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SEQ ID NO 4
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les 264; Conserv
                                           CTCAAGCAATTCTCCCCACCTCAGCCTCCCAAATAGCTGGGATCACTGGCACAAACCACCA 4659
                                                                                             GTTGCCTAGGCTGGAGTGCAGTGGCGCAATCTCGGCTCACTGCAACCTCTGCCTCTGGG 4599
                                                                                                                                   AGGCGTGAGCCACCGCGCCCGGC 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGCCCAGCTAA-TTTTGTATTTTTTGTAGAGACAGGGTTTCACCATGTTGCCCAGGCTGG 4718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTGCCTAGGCTGGAGTGCAGTGGCGCAATCTCGGCTCACTGCAACCTCTGCCTCTGCG 4599
TGCCCAGCTAA-TTTTGTATTTTTTGTAGAGACAGGGTTTCACCATGTTGCCCCAGGCTGG
                           TCCAAGCAATTGTCCAGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCGCGCACCACCA
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                                                                                GTTGCCCAAGCTGGAGTGGCACAATCTTGGCTCACTGCAACCTCTGCTTCCTGGG
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Pred. No. 5.8e-
0; Mismatches
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Pred. No. 5.8e-42;
0; Mismatches 58;
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nes 58;
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US-09-167-681-45
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US-09-167-681-45
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 45
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 3.5%;
Best Local Similarity 80.4%;
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LOCATION: (4827)...(4925)
NAME/KEY: CDS
LOCATION: (6322)...(6447)
NAME/KEY: CDS
LOCATION: (6543)...(6638)
NAME/KEY: CDS
LOCATION: (7137)...(7316)
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APPLICANT: Raftogianis, Rebecca B.
APPLICANT: Wood, Thomas C.
APPLICANT: Wood, Thomas C.
APPLICANT: Otterness, Diane M.
TITLE OF INVENTION: SULFOTRANSFERASE SEQUENCE VARIANTS
FILE REFERENCE: 07039/118001
CURRENT APPLICATION NUMBER: US/09/167,681A
CURRENT FILING DATE: 1998-10-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: CDS
LOCATION: (4361)...(4507)
NAME/KEY: CDS
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 4773
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                                                                                                            GATTACAGATGTGAGCCACCGCATCCAGCCCC 4804
                                    GCTTGGTCTCGAACTCCTGACCTCAGGTGATCCTGCTGCATCGACCTCCCAAAGTACTGG
                                                         GGCTGGTCTCAACCTCCTGGGCTCAAGCAATCCTCCTGCCTCGGCCTCCCCAAAGTGCTGG
                                                                                                                                              CCACCATGCCCAGCTAA-TTTTGTATTTTTTGTAGAGACAGGGTTTCACCATGTTGCCCA 4712
                                                                                                                                                                                                                        CCTGGGCTCAAGCAATTCTCCCACCTCAGCCTCCCAAATAGCTGGGATCACTGGCACAAA 4653
                                                                                                                                                                                                                                                           CACTCTGTTGCCCCAGGCTGGAGTGCAGTGGTGTGATCTTGGCTCACTGAAACCTCCGCCT
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US-08-451-777A-7
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 5971
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REGISTRATION NUMBER: 37,126
REFERENCE/DOCKET NUMBER: P51
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                              4596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 23-SEP-1994 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Human Galactokinase NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bergsma, Derk J.
APPLICANT: Stambolian, Dwight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 267; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 26-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: 709 Swedeland Road/UW2220 CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US94/10825
                CTGGTCTCAACCTCCTGGGCTCAAGCAATCCTCCTGCCTCGGCCTCCCAAAGTGCTGGGA 4774
                                                          ACCATGCCCAGCTAA-TTTTGTATTTTTGTAGAGACAGGGTTTCACCATGTTGCCCAGG
                                                                                                                             CAGGTTCAAGCAATTCTCCTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCGCCTGCC
                                                                                                                                              TGGGCTCAAGCAATTCTCCCCACCCTCAGCCTCCCAAATAGCTGGGATCACTGGCACAAACC
CTGGTCTCGAGCTCCTGACCTCAGGCAATCTGCCTGCCTCAGCTTCCCAAAGTGCTGGGA
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Pred. No. 9.3e-42;
0; Mismatches 65;
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US-08-451-778A-7
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
FRUGTH: 7676 base pairs
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 267; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Eagle, Alissa M.
REGISTRATION NUMBER: 37,126
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5364
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
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TITLE OF INVENTION: Human Galactokinase
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                               5851 CAGGTTCAAGCAATTCTCCTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCGCCCTGCC
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 709 Swedeland CITY: King of Prussia
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CTGGTCTCGAGCTCCTGACCTCAGGCAATCTGCCTGCCTCAGCTTCCCAAAGTGCTGGGA
                                                                ACGATGCCCGGCTAACTTTTGTATTTTTAGTAGAGACGGGGTTTCGCCATGTTGGCCAGG
                                                                                 ACCATGCCCAGCTAA-TTTTGTATTTTTTGTAGAGACAGGGTTTCACCATGTTGCCCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
EDNESS: double
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Pred. No. 9.3e-42;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 610-270-5364
TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                     4536
                                                                                                                                                                                                      5731
                                                                                                                                                                                                                                     FILING DATE: 23-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Eagle, Alissa M.
REGISTRATION NUMBER: 37,126
REFERENCE/DOCKET NUMBER: P50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA RE-BASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
5911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: 26-MAY-1
APPLICATION NUMBER: (
ETITION NUMBER: (
ETITION NUMBER)
               4656 ACCATGCCCAGCTAA-TTTTGTATTTTTTGTAGAGAGAGAGGGTTTCACCATGTTGCCCAGG 4714
                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                        Local Similarity
mes 267; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property
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                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                   TGGGCTCAAGCAATTCTCCCCACCTCAGCCTCCCAAATAGCTGGGATCACTGGCACAAAACC
                                                                                                                                                                                                   TTCTGTTGCCTAGGCTGGAGTGCAGTGGCGCAATCTCGGCTCACTGCAACCTCTGCCTCC 4595
ACGATGCCCGGCTAACTTTTGTATTTTTAGTAGAGGCGGGGTTTCGCCCATGTTGGCCAGG
                                                               CAGGTTCAAGCAATTCTCCTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCGCCTGCC
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Stambolian, Dwight
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                                                                                                                                      5791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5024
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MEDIUM TYPE: Floppy disk
5911
                4656 ACCATGCCCAGCTAA-TTTTGTATTTTTGTAGAGAGACAGGGTTTCACCATGTTGCCCAGG 4714
                                                                                                                                                                       4536 TTCTGTTGCCTAGGCTGGAGTGCAGTGGCGCAATCTCGGCTCACTGCAACCTCTGCCTCC 4595
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                    TTACAGGTGTGAGCCACCGCGCCCACCCATTCA 6063
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ACGATGCCCGGCTAACTTTTGTATTTTTAGTAGAGACGGGGTTTCGCCATGTTGGCCAGG
                                                                   CAGGTTCAAGCAATTCTCCTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCGCCTGCC
                                                                                   TGGGCTCAAGCAATTCTCCCCACCTCAGCCTCCCAAATAGCTGGGATCACTGGCACAAACC 4655
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King of Prussia
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80.2%; Pred. No. 9.3e-42;
tive 0; Mismatches 65;
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US-08-257-963B-11
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                                                                    Matches
                                                                                    Query Match
Best Local :
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                            4495 TTTTCTTTTTTTTTTTTTTAATGTGAGACAGGATCTCATTCTGTTGCCTAGGCTGGA 4554
                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: UFILING DATE: CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy Disk
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                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                               MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 07/952,796 FILING DATE: 24-SEPT-1992 ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Chader, Gerald J.; Becerra, APPLICANT: Patricia; Schwartz, Joan P.; APPLICANT: Taniwaki, Takayuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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532 TTTTTTTTTTTTTTTTNNNCTTTCTGAGACGGAGTCTCGCTTTGTCNCCAAGGCTGGA 591
                                                                                                                                                 IDENTIFICATION METHOD:
OTHER INFORMATION: 2
OTHER INFORMATION: pr
                                                                                                                                                                                                                                                                                                             TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Unknown
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                                                                                                                                                                                                                                                           ORGANISM:
                                                                                                                                                                                                           LOCATION
                                                                                                                                                                                                                           NAME/KEY: JT108
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                                                                                    Similarity
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                                                                    Conservative
                                                                                                                                                                                                                                                             Human
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212) 751-6849
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                                                                               Score 216.8; DB 2;
Pred. No. 5.4e-42;
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                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                            TELEFAX: (212) 751-6849 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/257
FILING DATE: 07-7UN-1994
PRIOR APPLICATION DATA:
APPLICATION UMBER: 07/952
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                           REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Chader, Gerald J.; Rodriguez, APPLICANT: Ignacio R.; Mazuruk, Krzysztof; APPLICANT: Tombran-Tink, Joyce TITLE OF INVENTION: PIGMENT EPITHELIUM TITLE OF INVENTION: DERIVED FACTON: CHARACTURE OF INVENTION: ORGANIZATION AND SEQUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: WORDPERFECT CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy Disk
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                   FEATURE
                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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CITY: New York
STATE: New York
                                  ORGANISM:
                                                                                        TOPOLOGY:
                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
NAME/KEY:
                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                   NAME:
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                                                                                                                       Nucleic Acid
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                                                                                                                                           1988 Base Pairs
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                                  Human
                                                                                      Unknown
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                                                                                                                                                                                                              (212)
                                                                      Genomic DNA
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                                                                                                         Double
                                                                                                                                                                                                                758-4800
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DERIVED FACTOR: CHARACTERIZATION GENOMIC
ORGANIZATION AND SEQUENCE OF THE PEDF GENE
                                                                                                                                                                                                                                                                                                                                      07/952,796
                                                                                                                                                                                                                                                                                                                                                                                        08/257,963
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PCT-US95-07201-11
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Best Local Sim.
Matches 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application PC/TUS9507201 GENERAL INFORMATION:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/36
FILING DATE: 30-DEC-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07:
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Chader, Gerald J.; Becerra, Sofia
APPLICANT: Patricia; Schwartz, Joan P.;
APPLICANT: Taniwaki, Takayuki
TITLE OF INVENTION: PIGMENT EPITHELIUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
NUMBER OF SEQUENCES: 43
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MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4615 CACCTCAGCCTCCCAAATAGCTGGGATCACTGGCACAAACCACCATGCCCAGCTAA-TTT 4673
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                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 345 Park
CITY: New York
STATE: New York
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OTHER INFORMATION: 2 kb PCR product using
OTHER INFORMATION: primers, SEQ ID: 13 and 14; Also referred
OTHER INFORMATION: to as JT108
                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                    USA
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82.8%;
                                                                                                                                            08/367,841
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Pred. No. 5.4e-42;
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US-08-520-373D-5
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                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/08520373D Patent No. 6451763
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Best Local Similarity
Matches 256; Conserv
CURRENT APPLICATION NUMBER: US/08/520,373D CURRENT FILING DATE: 1995-08-29 PRIOR APPLICATION NUMBER: 08/377,710 PRIOR FILING DATE: 1995-01-25 PRIOR APPLICATION NUMBER: 08/279,979 PRIOR APPLICATION NUMBER: 07/894,215
                                                                                                                                             APPLICANT: Steele, Fintan R
APPLICANT: Chader, Gerald J
APPLICANT: Becerra, Sofia P
APPLICANT: Johnson, Lincoln V
APPLICANT: Rodriquez, Ignacio R
TITLE OF INVENTION: RETINAL PIGMENTED EPITHELIUM DERIVED NEUROTROPIC
FILE REFERENCE: 2026-4203US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1988 Base Pairs
                                                                                                                                                                                                                               APPLICANT: Tombran-Tink, Joyce
APPLICANT: Steele, Fintan R
APPLICANT: Chader, Gerald J
APPLICANT: Becerra, Sofia P
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OTHER INFORMATION: 2 kb PCR product using
OTHER INFORMATION: primers, SEQ ID: 13 and 14;
OTHER INFORMATION: to as JT108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCCTCAGCCTCCAGAGTAGCTGGGATTACAGGCACCTGCCATCATGCCCAGCTAATTTT
                                                                                                                                                                                                                                                                                                                     INFORMATION:
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Pred. No. 5.4e-42;
Pred. No. 5.4e-42;
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PRIOR FILING DATE: 1992-06-04
PRIOR APPLICATION NUMBER: 07/
PRIOR FILING DATE: 1992-09-24
NUMBER OF SEQ ID NOS: 34

1992-06-04 NUMBER: 07/952,796

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; OTHER INFORMATION: n = a US-08*520-373D-5
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                                                                                                                                                       Sequence 43, Application US/08367841A Patent No. 6319687
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Best Local Similarity 82.8
Conservative
                                                                                                                                    Patent No. 6319687
GENERAL INFORMATION:
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LOCATION: (1984)..(2187)
NAME/KEY: exon
LOCATION: (5170)..(5256)
NAME/KEY: intron
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LOCATION:
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OTHER INFORMATION: EXON 5170-5255; INTRON 162-1141; INTRON
OTHER INFORMATION: 1298-1983; INTRON 2188-5169; CDS 35-161; CDS
OTHER INFORMATION: 1142-1297; CDS 1984-2187; CDS 5170-5255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (35)..(160)
NAME/KEY: exon
LOCATION: (1142)..(1297)
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ORGANISM: HUMAN
FEATURE:
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                          APPLICANT: Chader, Gerald J.; Rodriguez, APPLICANT: Ignacdo R.; Mazuruk, Krzysztof; APPLICANT: Tombran-Tink, Joyce TITLE OF INVENTION: PIGMENT EPITHELIUM TITLE OF INVENTION: DERIVED FACTOR: CHARACTITLE OF INVENTION: ORGANIZATION AND SEQUE
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CORRESPONDENCE
                 NUMBER OF SEQUENCES:
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Pred. No. 8.6e-42;
0; Mismatches 52;
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Best Local Similarity
Matches 256; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 07/9:
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/2:
FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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CITY: New York
STATE: New York
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OTHER INFORMATION: full leng
OTHER INFORMATION: sequence
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TOPOLOGY: Unl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
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                                                               CTCAAGCGATCCACCGCCTTGGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCG
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                               CATCCAGCC 4802
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Pred. No. 1.7e-41
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Job time : 724 secs

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Title:
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Maximum Match 100%
Listing first 45 summaries
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/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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    US-09-899-569A-3
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US-09-822-217-362
US-09-813-263-362
US-09-815-343-613-362
US-09-815-343-613-365
US-09-815-343-393
US-09-867-701-3866
US-09-867-701-9866
US-09-764-877-2607
US-09-764-877-2607
US-09-962-436-281
US-09-964-824A-27
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2605, Ap
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2607, App
273, App
            1109, Ap
1108, Ap
295, App
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APPLICANT: NO. US20030142003Albert Schweifer
APPLICANT: Marwa Scherl-Mostageer
APPLICANT: Wolfgang Sommergruber
APPLICANT: Wolfgang Sommergruber
APPLICANT: Wolfgang Sommergruber
APPLICANT: Wolfgang Sommergruber
APPLICANT: Reger Abseher
TITLE OF INVENTION: Tumorassoziiertes Antigen (B345)
FILE REFERENCE: 0652.2280001
CURRENT APPLICATION NUMBER: US/09/899,569A
CURRENT FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: DE 100 33 080.0
PRIOR APPLICATION NUMBER: DE 101 19 294.0
PRIOR APPLICATION NUMBER: US 60/243,158
PRIOR APPLICATION WIMBER: US 60/243,158
PRIOR APPLICATION NUMBER: US 60/243,158
PRIOR APPLICATION NUMBER: US 60/243,158
PRIOR APPLICATION NUMBER: US 60/297,747
PRIOR FILING DATE: 2001-06-14
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.1
                                   SEQ ID NO 3
LENGTH: 6163
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
FEATURE:
LOCATION: (1)..(282)
NAME/KEY: 5'UTR
LOCATION: (1)..(282)
NAME/KEY: GC_signal
LOCATION: (147)..(157)
NAME/KEY: GL_Signal
LOCATION: (201)..(209)
COTHER INFORMATION: cap signal; TI
NAME/KEY: 3'UTR
LOCATION: (2794)..(6163)
LOCATION: (2794)..(6163)
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LOCATION: (283)..(2793)
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1 TTTGAGGGTGAAGGCTCAGCAACCCTGATGTCTGCCAACTACCCAGAAGGCTTCCCTGAG 1020 	1 TCCGGCTTCAGCATTGCAAACCGCTCATCTATAAAACGTCTGTGCATCATCCAGGTCTGTG 960 	1 AAGATGCAAGAAGGAGTGAAAATGGCCTTACACCTCCCATGGTTCCACCCCAGAAATGTC 900	1 ATCGATGCCACCGTGGTCAGGATCGGAACCTTCTGCAGCAATGGCACTGTGTCCCGGATC 840	1 AGGCAGATCGGTCCGGGTGAGAGCTGCCCAGACGGAGTCACTCAC	1 TGGGATGTCAAAGCTCATAAGAGCATCGGTTTAGAGCTGCAGTTTTCCATCCCTCGCCTG 720 	1 GGGGAGGTTCAGCCTTCAGCCCTCGACATCGTTGTTGCCCTACCCTCAACAGAACTTTCATC 660 	1 AATCACTTTGTCATAGAGATCCAGAAAAATATTGACTGTATGTCAGGCCCATGTCCCTTTT 600	1 ATGTTGTCCATCAAGTCTGGAGAAAGAATAGTCTTTACCTTTAGCTGCCAGAGTCCTGAG 540	1 GGGACCCCGACTCTGCTGGCAAAACCCTGTTACATCGTCATTTCTAAAAGACATATAAACC 480 	1 GCAGAAGCTTTTGAGATTGCTCTGCCACGAGAAAGCAACATTACAGTTCTCATAAAGCTG 420 	1 GGGGTCTCTATCGCACTGCTAGGGGTTCTGCTGCTGCGGGGGGGG	1 CCACCGTCGTTTTCCCCCACCGAGGCCGAGGCGTCCCGGAGTCATGGCCGGCC	1 GTGAGTGAGCCAGGGCGGAGCGCAGCTGCGCCGGGGTTGGGGCGCCTGGGGGCCGCCGCTCC 240	1 CGGGTCAGCTCGCGATCCTGCTGCGCAGGGCGGGGCTCGGGCCGGTCCGCCCGC	1 TGGGAGGGAGAGGCGGTCGCTGAGGCAGGAAGAGGAGGAGGAGAGAGA	1 CCAACGCCGCAATGGGGAGTAGTAGGGACCCAGCAACCCGGTGCCGGGAGCCCTGCACCC 60	Match 100.0%; Score 6163; DB 10; Length 6163; Local Similarity 100.0%; Pred. No. 0; Nes 6163; Conservative 0; Mismatches 0; Indels 0; Gaps
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1021 GATGAGCTCATGACGTGGCAGTTTGTCGTTY 1081 CTCAACTTCAACCTCTCCAACTGTGAGGTG 1081 CTCAACTTCAACCTCTCCAACTGTGAGGGG 1141 GGCTCCACTTCAACCTCTCCAACTGTGAGAGG 1141 GGCTCCACCTCTCAACCTCTCCAACTGTGAGAGGG 1141 GGCTCCACCTCTCAACCTCTCCAACTGTGAGAGGG 1141 GGCTCCACCTCTCAACCTCTCTCTGCAAGGCTGTT 1201 GGGAACTTCAACCTCTCTCTGCAAGGCTGTT 1201 GGGAACTTCAACCTCTCTCTGCAAGGCTGTT 1201 GGGAACTTCAACCTCTCTCTGCAAGGCTGTT 1201 GGGAACTTCAACCTCTCTCTGCAAGGCTGTT 1201 GGGAACTTCAACCTCTCTCTGCAAGGCTGTT 1201 GGGAACTTCAACCTCTCTTGGTCCAAGGCTGTT 1201 GGGAACTTCAACCTCTCTTGGTCCAAGGCTGTT 1201 GTTGACTTGAGTAATGAGGGAGCCATGTCAA 1321 GTTGACTTGAGTAATGAGCGAGCCATGTCAA 1321 GTTGACTTGAGTAATGAGCGAGCCATGTCAA 1321 GTTGACTTGAGTAATGAGCGAGCCATGTCAA 1321 GTTGACTTGAGTTATGTCCCTGGCTGTTTCGTG 1321 GTTGACTTGAGTTATGTCCCTGGCTGTTTCGTG 1321 GTTGACTTGAGTTATGTCCCTGGCTGTTTCGTG 1321 GTTGACTTGAGTTTGTCCCTAAACACAAA 1441 CTCACCCTTGACATCTGGGCTCCAAACACAAAA 1441 CTCACCCTTGACATCTGGGCTCCAAACACCAAAA 1441 CTCACCCTTGACATCTGGGTTCCCAAGGACAGCA 1501 TCCTGTGGATGAATGTGGAAAAAACCATAAGCT 1501 CTGTGGATGAATGTGGAAAAAACCATAAGCT 1501 CTGTGGATGAAGTTGTGGAAAAAACCATAAGCT 1501 CTGTGGATGAAGTGTGGGTGCCCAAGGAACATCAT 1501 CTGTGGATGAAGCTGTGTGGTGCCCAAGGAACATCATAAGCT 1501 TCCTGGAAGCTGCTGGTGCCCAAGGAACATCCTGGGT 1511	i i	TGGTCTGCCAGACAGGGCGCGC AGATCTTCAGCCTGGACGAGG	2101	Оy	
1021 GATGAGCTCANGACGTGCAATTTGTCGTTCCTGCACACCTGCACCTGCACCTGCACCTGCACCTGCACCTGCACACGTGTTCAACCTTGAACAGGAAGAAGGAAG	= 5	TGCCTGACTTTCTTTAAGGAGCGGAGCGGCGTGGTCTGCCAGACAGGGCGCGCAT	2 2	Dy Oy	
1021 GATGAGCTCATGACGTGCAATTGTCGTTCCTCCACACCTGCACACCCACC	8=		.98	Db	
1021 GATGAGCTCATGACGTGCCACTTTGCTGCTCCACACCTGCTGCACCTTGCTGCACCTTGCTGCACCTTGCTGCACCTTGCACCTTGCACCTTGCTGCACCTTGCTGCACCTTGCTGCACCTTGCTGCACCTTGCTGCACCTTGCTGCACCTTGCTGCACCTTGCTGCACCTTGCACGTGGCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGCGGGTTGCTACTGCACCTTCCACCTTCCAACTTGCAACTTCACCTTGCAACTTGCAACTTGCAACTTCACCTTGCAACTTCACCTGTGAAGGAGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAG	ର୍	CCTGCCATCCCTCACCTCTGTGTCCTGGAACATCAGCGTGCCCAGAGACCAGG	٠,	Ωу	
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1021 GATGAGCTCAFGACGTTGGCAGTTTGTCGTTCCTCGACACCTGCCTCCTCTCACACCTTCCTGCACACCTCCTCCAACCTTGTGTGTTCTCTGCAACCTTCCAACCTTGCAGTTTGTCGTTTGTCTTCTCAACCTTCCAACCTTGTGAGAGGAAGGA		CC10	62	Qу	
1021 GATGAGCTCAHGACGTGCAGTTTGTCGTTCCTCGCACCCTGCCACCTTGCCTICCTGCACCTCCTGCACCTCCTGCACCTCCTGCACCTCTCCACCTTGCACCTTGCACCTTGCACCTTGCACCTTGCACCTTGCACCTTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG		TCCTACTCACTCCAGGTGCCCAGTGACATCCTCCACCTGCCTG	.56	Qу Дъ	
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240	1 CTCTCACTGGGGTCCCCCAGGATGAAAACGACAATGTGCCTTTTTATTATTATTTAT	Qу 318:
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120 120	1 AGAGAGGCCTGAGTCACCTAGCATAGGGTTGCAGCAAGCCCTGGATTCAGAGTGTTAAAC 3	Qу 306; Db 306;
060	1 CATGACAGCTCATGTGCTCCTCAACTTAGGCTGTGCGGTTAGCCAGCC	оу 300: рь 300:
000	1 TCAGTGGACTCATTCTAAGGGCAAGACATTGAAAATGATGAATTCCAATCTGGATACAGT 3	Qy 294 Db 294
940	1 GAGGAATTATACAGAAGGAACAGCAGGAGGTTTTCCTGGACACCGCCAACTTCACATTGC 2	Qy 288 Db 288
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RESULT 2
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RESULT 2
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; Sequence 1, Application US/09899569A
; Sequence 1, Application US/09899569A
; Patent NO. US20020142003A1
; GENERAL INFORMATION:
 APPLICANT: NO. US20020142003A1bert Schweifer
 APPLICANT: Wolfgang Sommergruber
 APPLICANT: Wolfgang Sommergruber
 APPLICANT: Wolfgang Sommergruber
 APPLICANT: Noger Abseher
 TITLE OF INVENTION: Tumorassoziiertes Antigen (B345)
 FILE REFERENCE: 0652.2280001
; CURRENT APPLICATION NUMBER: US/09/899,569A
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: DE 100 33 080.0
; PRIOR TILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: DE 101 19 294.0
; PRIOR APPLICATION NUMBER: US 60/243,158
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 60/243,158
; PRIOR APPLICATION NUMBER: US 60/297,747

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SOFTWARE: PATENTIN V
SEQ ID NO 1
LENGTH: 5897
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (5348)...(5348)
OTHER INFORMATION: n is any nu
NAME/KEY: misc_feature
LOCATION: (5360)...(5360)
OTHER INFORMATION: n is any nu
NAME/KEY: misc_feature
LOCATION: (5425)...(5425)
OTHER INFORMATION: n is any nu
NAME/KEY: misc_feature
LOCATION: (5438)...(5438)
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NAME/KEY: 5'UTR
LOCATION: (215)..(214)
NAME/KEY: 5'UTR
LOCATION: (215)..(2464)
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LOCATION: (2465)..(5897)
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Best Local Similarity 99.0
Matches 5865; Conservative
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- 3	CTGTCCTCCCTCCCACCACCATATGCTCCAGGGC 2630	GCCGTTCCAGGGCACCATGGGGGTCC	2571 2304	유 성
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- 3	CCATGTGTATGCAGTCATCGAGGACACCATGGTATA 2510	GAAAGGGCGAAAGGACAATGACTO	2451 2184	용 성
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3710 3443	TTTAAATATATACCAAACAGTGGCCCCCTGCATTAGTTTTCTGTTGCCACTGCAACCCAT	3651 3384	Qy Db	
3650 3383	TGCAGCAATACTTTGACATTTAAAGAGAAATTTAAGAGAATATTCTCATCCTCTAAAAATG	3591 3324	Оу	
3590 3323	GTCCTATAGTCCTAGCAATAAGAGAAATTTCCTCAAGTTTCCATGTGCGGTTCTCCTAGC	3531 3264	Оу	
3530 3263	CCTGATTCTCTAGGTCGGTTCGTGGTTATCCCATTGTGGAAATTCATCTTGAATCCCATT	3471 3204	Qy Db	
3470 3203	CCAGAAAAGAATGTGTGTGTTTGAGCAGCATTGACACATATCTGCTTTGATAAGAGACTT	3411 3144	Qy	
3410 3143	ACCGCTAGATAAACGTGTGCCTGTCCCCCAGGTGGTGGGAATAATTTACAATCTGTCCAA	3351	Qy Db	
3350 3083	ACCTGACTTAGTAATAACTCATACTAACTGGTTTGGATGCCTGGGTTGTGACTTCTACTG	3291 3024	Qy	
3290 3023	ATTTATTTGGTGGTCCTGTGTTATTTAAGAGATCAAATGTATAACCACCTAGCTCTTTTC	3231 2964	Оy	
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                                                                             AGGCTTTGGGATACAAGTTCTTCCTCCTTCATTTGATGCCGTGCACTGTGTGAAGCAGAT
                                      AGTGCTTCGGCTACTTGTCCCCTGGTTCAGTAGAGGCCCCGGTTTCCCCAGTTGTTGACTG
                                                                                                ACTGGTCTCTAATGCTGTGGTCATTGCACAGAAGGGAAAGGTCTCAAGGAAGAGTCAACT
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ANTGGTCTCTAATGNTGTGGTCATTGCACAGAAGGGAAAGGTCTCAAGGAAGAGTCAACT
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NESULT 3
US-09-922-217-362
Sequence 362, Application US/09922217
Patent No. US20020076414A1
GENERAL INFORMATION:
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Wang, Tongtong
APPLICANT: Jiang, Yuqiu

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APPLICANT: Smith, Carole Lynn
APPLICANT: King, Gordon E.
APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
TITLE OF INVENTION: OF COLON CANCER AND METHODS FO!
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FBStSEQ for Windows Version 4.0
                                                                                                         RESULT 4
US-09-833-263-362
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                                                                       Sequence 362, Application US/09833263 Patent No. US20020110547A1 GENERAL INFORMATION:
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Best Local Similarity 99.8%;
Matches 543; Conservative
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LENGTH: 544
APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Stolk, John
APPLICANT: Meagher, Madeleine J.
TITLE OF INVENTION: COMPOUNDS FOR
TITLE OF INVENTION: DIAGNOSIS OF
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Pred. No. 2.1e-102;
0; Mismatches 1;
 IMMUNOTHERAPY AND I
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S FOR THEIR USE
  METHODS
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Sequence 1335, Application US/09815343
Patent No. US20010055596A1
GENERAL INFORMATION:
APPLICANT: Meagher, Madeleine
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF COLON CANC
FILE REFERENCE: 210121.504
CURRENT APPLICATION UNMBER: US/09/815,343
CURRENT FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1335
LENGTH: 541
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US-09-815-343-1335/c
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; TYPE: DNA
; ORGANISM: Homo sapien
US-09-833-263-362
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CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 362
LENGTH: 544
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Best Local Similarity
Matches 543; Conserv
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Pred. No. 2.1e-102;
0; Mismatches 1;
                                                                                            AND METHODS F
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Sequence 666, Application US/09815343

Patent No. US20010055596A1

GENERAL INFORMATION:
APPLICANT: Meagher, Madeleine
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.504
CURRENT APPLICATION NUMBER: US/09/815,343
CURRENT FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 1556
SOFTMARE: FBStSEQ for Windows Version 4.0
SEQ ID NO 666
LENGTH: 636
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US-09-815-343-666
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Best Local :
NAME/KEY: misc_feature LOCATION: (1)...(636) OTHER INFORMATION: n -09-815-343-666
                                                                   ORGANISM: Homo sapien
                                                                                     TYPE: DNA
                                                       FEATURE:
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Pred. No. 1.8e-100;
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TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRE TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRE FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/879,536
CURRENT FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: US 60/088,801
PRIOR FILING DATE: 1990-06-10
NUMBER OF SEQ ID NOS: 850
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 370
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Best Local Similarity
Matches 536; Conserv
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APPLICANT:
APPLICANT:
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                                                                                                                                      Ford, Donna M.
Lewis, Marcia E.
Monahan, John E.
Schlegel, Robert
                                                                                                                                                                                          Burgess, Christopher (
Bushnell, Steven E.
Carroll III, Eddie
Catino, Theodore J.
Derti, Adnan
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98.3%;
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Pred. No. 2.6e-98;
0; Mismatches 8
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RESULT 8
US-09-815-343-393
US-09-815-343-393
; Sequence 393, Application US/09815343
; Patent No. US20010055596A1
; GENERAL INFORMATION:
; APPLICANT: Meagher, Madeleine
; APPLICANT: Xu, Jiangchun
; APPLICANT: Xing, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR T
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.504
; CURRENT APPLICATION NUMBER: US/09/815,343
; CURRENT FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 1556
; NUMBER OF SEQ ID NOS: 1556
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; LOCATION: (1)...(636)
; OTHER INFORMATION: n = A,T,C
US-09-879-536-370
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Best Local Similarity 90.3%;
Matches 577; Conservative
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TYPE: DNA
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Pred. No. 1.9e-91;
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CURRENT APPLICATION NUMBER: US/09/867,701
COURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 3051
LENGTH: 348
TYPE: DNA
ORGANISM: Homo sapien
US-09-867-701-3051
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                                                                                                                                                                                                                           Sequence 3051, Application Patent No. US20020132237A1 GENERAL INFORMATION:
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Best Local Similarity 94.8%;
Matches 509; Conservative
                                                                                                                                 APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
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TYPE: DNA
ORGANISM: Homo
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TH: 535
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Pred. No. 5.2e-90;
D; Mismatches 26;
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69

Score

DB 10;

Length

5875

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Sequence 9866, Application US/09867701

Patent NO. US2002013237A1

GENERAL INFORMATION:
APPLICANT: Aglate, Paul A.
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 210121.497

CURRENT APPLICATION NUMBER: US/09/867,701

CURRENT APPLICATION NUMBER: US/09/867,701

CURRENT APPLICATION NUMBER: US/09/867,701

CURRENT APPLICATION SAND DIAGNOSIS OF OVARIAN CANCER PROFESSOR OF SEQ ID NOS: 10912

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 9866

LENCTH: 339
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; ORGANISM: Homo sapien
US-09-867-701-9866
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Matches 339; Conserv
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Pred. No. 9.5e-61;
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2605
LENGTH: 5157
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-877-2605
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US-09-764-877-2605/c
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                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PCOO5
                           Prior application data removed - refer to NUMBER OF SEQ ID NOS: 4031
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2607
LENGTH: 5199
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                  Sequence 2607, Application US/09764877 Patent No. US20020147140A1
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Best Local Similarity
Matches 279; Conserv
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC005
                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
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CURRENT FILING DATE: 2001-01-17
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NAME/KEY: SITE LOCATION: (233)
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Pred. No. 4.1e-38;
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NAME/KEY: SITE
LOCATION: (2810)
OTHER INFORMATION: n
NAME/KEY: SITE
LOCATION: (2833)
OTHER INFORMATION: n
NAME/KEY: SITE
LOCATION: (2834)
OTHER INFORMATION: n
NAME/KEY: SITE
LOCATION: (2834)
OTHER INFORMATION: n
NAME/KEY: SITE
LOCATION: (2856)
OTHER INFORMATION: n
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LOCATION: (918)
OTHER INFORMATION: n
NAME/KEY: SITE
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OTHER INFORMATION: n
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LOCATION: (1035)
OTHER INFORMATION: n
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LOCATION: (2878)
OTHER INFORMATION: :
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LOCATION: (5140)
OTHER INFORMATION:
US-09-764-877-2607
                                                                                                                                                                                                                                    Query Match
Best Local Similarity 77.7
Matches 279; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: SITE
LOCATION: (3472)
OTHER INFORMATION: I
NAME/KEY: SITE
LOCATION: (4420)
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                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (4618)
OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: (509
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LOCATION: (4570)
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LOCATION: (4438)
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                                                 TCTGCCTCCTGGGCTCAAGCAATTCTCCCCACCTCAGCCTCCCAAATAGCTGGGATCACTG
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TGTTGGGATTACAGGCGTGAGCCACCGCGCCCCAGCCTCCCTTCTTTTCTTATTGCCAAT
                                                                             TCTGCCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCTGAGTAGCTGGGATTACAG
                                                                                                                                                             AGAGTCTCGCACTGTTGTCCAGTCTGGAGTGCAATGGTGCAATCTCGACTCACTGTAACC
                                      TGGTCAGGCTGGTCTGGAACTCCTGACCTCAGGTGATCCACCTGCCTTGGCCTCCCAAAG
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Pred. No. 4.1e-38;
D; Mismatches 80
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RESULT 13
US-09-962-436-281/c
; Sequence 281, Application US/09962436
; Patent No. US20020081301A1

GENERAL INFORMATION:
APPLICANT: Soppet, Daniel
TITLE OF INVENTION: Cancer Gene Determinat
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-75
CURRENT APPLICATION NUMBER: US/09/962,436
CURRENT FILING DATE: 2001-09-25

Determination

and

Therapeutic

Screening

Using

Sign

PRIOR APPLICATION

NUMBER: US/60/235,082

PRIOR FILING DATE: 2000-09-25

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PRIOR APPLICATION NUMBER: US/60/234,924
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 568
SOFTWARE: Patentin version 3.0
SEQ ID NO 281
LENGTH: 167343
TYPE: DNA
ORGANISM: Homo sapiens
US-09-962-436-281
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Patent No. US20020102531A1
GENERAL INFORMATION:
APPLICANT: HORRIGAN, Stephen
TITLE OF INVENTION: Cancer Gene Determination
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-73
                                                                                                                                                                                                            SOFTWARE: Patentin
SEQ ID NO 273
LENGTH: 167343
                                                                                            Query Match
Best Local (
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Best Local Similarity
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PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,028
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 583
                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/964,824A CURRENT FILING DATE: 2001-09-27 PRIOR APPLICATION NUMBER: US/60/236,033 PRIOR FILING DATE: 2000-09-28
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                4495 TITTCTTTTTTTTTTTTTTTTTAATGTGAGACAGGATCTCATTCTGTTTGCCTAGGCTGGA 4554
                                                                          Local Similarity
nes 271; Conserv
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                                                                                            Score 230.8;
Pred. No. 1.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.7%;
Best Local Similarity 78.8%;
Matches 282; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/982,091A CURRENT FILING DATE: 2002-10-17 PRIOR APPLICATION NUMBER: US 60/241,246 PRIOR ETILING DATE: 2000-10-17 NUMBER OF SEQ ID NOS: 12 SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
APPLICANT: KUMAGAI, AKİKO
APPLICANT: DÜNPHY, WİLLİAM
TITLE OF INVENTION: CLASPIN PROTEINS AND METHODS
FILE REFERENCE: CIT1320-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151949 TGCCTCAGCCTCCCCAGTAGCTGGGATTACAGGCACATGCCCACCACCCAGCTAATTTT 151890
                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
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CCGCCTCCGCCTCCCAAAGTGCTGGGGTTACAGGCGTGAGCCACCGCACCCGGCCTCA 55327
                                                                                                                      AGACAGGGTTTCACCATGTTGCCCAGGCTGGTCTCAACCTCCTGGGCTCAAGCAATCCTC 4747
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                                                                                AGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTGACCTCAGGTTATCTGC
                                                                                                                                                            AAGTAGCTGGGATTACAGGCGCCCGCCACCAAGCCCGGCTAATTTTTGTATTTTAGTAG
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Pred. No. 1.2e-36;
0; Mismatches 75;
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Maximum Match 100%
Listing first 45 summaries
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Mammalia; Eutheria;
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ALIGNMENTS

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1. .2225
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Gunaratne, P.H., Garcia, A.M., Lu,
Yoon, V.S., Kowis, C.R., Lawrence,
Richards, S., Gibbs, R.A.
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/db_xref="taxon:10090"
/map="CZECH II"
/clone="IMAGE:4014852"
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AB033417 Hon
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Department of Reproductive Physiology and Endocrinology
Medical Institute of Bioregulation, Kyushu University
Tsurumihara 4546, Beppu, Oita 874-0838, Japan
Tel: 0977-27-1660
Fax: 0977-27-1661
                                                                                                                                                                                                                                                           Homo sapiens Euthazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. 1 (bases 1 to 933)
                                                                                                                                                                                                                          Unpublished (1999)
                                                                                                                                                                                                                                   Biological function unknown
                                                                                                                                                                                                                                               Zhou, Y., Kato, H. and Wake, N.
                                                                                                                                  yzhou@tsurumi.beppu.kyushu-u.ac.jp.
Location/Qualifiers
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                              /clone_lib="Homo sapiens skov"
/cell_type="ovarian cancer"
/cell_line="skov"
/note="Buessow, K. et al., 1998,
26(21): 5007-5008"
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Department of Reproductive Physiology and Endocrinology Medical Institute of Bioregulation, Kyushu University Tsurumihara 4546, Beppu, Oita 874-0838, Japan
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Mammalla; Eutherla; Primates; C:
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, I
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Location/Qualifiers
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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Tissue Procurement: ATCC
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AGENCOURT_8778970 NIH_MGC_42
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found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM2388 row: b column: 13 High quality sequence stop: 702. Location/Qualifiers
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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CDNA Library Arrayed by: The I.M. G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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//clone_lib="NiH_MGC_110"
//tissue_type="ductal carcinoma, cell line"
//lab_host="DH10B (phage-resistant)"
//note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
/note="Index pancreas; Vector: pOTB7; Site_1: XhoI;
// Site_2: EORI; CDNA made by oligo-dT priming.

Site_2: EORI; CDNA made by oligo-dT priming.

Site_2: EORI; CDNA made by oligo-dT priming.

Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
/clone="IMAGE:6248364"
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information ca
                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, M
Unpublished (1999)
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Mammalia; Eutheria; Primates;
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/clone="IMAGE:6208223"
/clone_lib="NIH_MGC_110"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site
Site_2: EcoRI; cDNA made by oligo-dT primir
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Note: this is a NIH_MCC Library."
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                                                         GAACATGGCGGGGAACTTCAACCTCTCTCTGCAAGGCTGTGACCAAGATGCCCAAAGTCC
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EST.
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Email: cgapbs r@mail.nih.gov

Tissue Procurement: DCTD/DTP/Gazdar

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lnl.gov
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AGENCOURT_8817950 NIH_MGC_18
5', mRNA sequence.
BO0517276
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High quality sequence stop: 719.
Location/Qualifiers
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1 (bases 1 to 984)
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National Institutes of Health, Mammalian
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/clone="IMAGE:6422238"
/clone="Ib="NIH_MGC_18"
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/tlssue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Corgan: lung; Vector: poTB7; Site_1: XhoI; Site_2:
/note="CORGAC This ites using the following 5' adaptor:
GCCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

38 a 301 c 247 g 197 t 1 others
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0; Mismatches 26;
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Mammalia; Eutheria; Primates; Catarrhini; H
1 (bases 1 to 871)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Ge
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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/lab_host="hHlOB (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming
Directionally cloned into EcoRI/XhoI sites using the
Directionally cloned into EcoRI/XhoI sites using the
following 5 adaptor: GGCAGGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
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Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/ILML at:
http://image.llnl.gov
plate: LLAM9669 row: f column: 01
High quality sequence stop: 724.
Location/Qualifiers
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Tissue Procurement: DCTD/DTP/Gazdar
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National Institutes of Health, Mammalian
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601486503F1 NIH_MGC_69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
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/clone_lib="NIH_MGC_69"
/clone_lib="NIH_MGC_69"
/Lissue_type="large cell carcinoma, undifferentiated"
/Lab_host="DH108 (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
Technologies."
a 329 c 312 g 250 t
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/db_xref="taxon:9606"
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602451816F1 NIH_MGC_14 Homo
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov o column: 03
High quality sequence stop: 699.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Contact: Robert Strausberg, Ph.
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National Institutes of Health, Mammalian
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1 (bases 1 to 851)
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/clone="IMAGE:4590554"
/clone_lib="NIH_MGC_14"
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TGTTACATCGTCATTTCTAAAAGACATATAACCATGTTGTCCATCAAGTCTGGAGAAAGA
                                                                          GGCCTTACACCTCCCATGGTTCCACCCCAGAAATGTCTCCGGCTTCAGCATTGCAAACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATATTGACTGTATGTCAGGCCCATGTCCTTTTGGGGAGGTTCAGCTTCAGCCCTCGACA
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GTCATTTATAAAAAAGTTGTGCTATCGCTTGGGTTGAGGGTGAAGG
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                                      CTCATCTATAAAACGTCTGTGCATCATCGAGTCTGTGTTTGAGGG
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Pred. No. 9.4e-89;
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IMAGE: 4442127

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ORGANISM
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Best Local Sim
Matches 742;
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                                           TTTATTGTAATGAAAAAGAAAGACTGGGATTAATCTCTAATCAGGTGAGTAGACCATGAG
ACAGGGATGTTTTGTTTAGCTTGCGGACTCTAACACTT-AAAAAAACCCCAGATCAGAAG 4215
                                                                                                                                                                                                                                                                                                                                                                                                                                 CAAGACAACATAGCCACAGGTGGGGATTAGGACCAGGACATCTTTGGGGTGCTGTTATTC 4096
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                                                                                                                                  TCACTTCCCACAATGAGGCTAAGTGTTTGTTTCTACTGATCAATGCCCCTGCAGGTTGCA 4395
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                                                                                                                                                                                                                                                                                    High
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10214 row: f column: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      National Institutes of Health, Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 779)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="adenocarcinoma, cell line"
/lab_host="DHIOB (phage-resistant)"
/note="Organ: liver; Vector: pcWv-SpORT6; Site_1: Noti;
Site_2: Sali; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies
Note: this is a NHH_MGC Library."

a 215 c 161 g 218 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4442127"
/clone_lib="NIH_MGC_90"
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Primates;
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Pred. No. 3.2e-86;
0; Mismatches 23
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Best Local Sim:
Matches 742;
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                                                               GTTCCCCATGTTTCGCCAGGTTGTCTCAACCTCCTGGGCTCAAGCAATCTTC
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Mammalia; Eutheria; Rodentia; Sc
1 (bases 1 to 977)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: ResGen, Invitrogen Corp CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bloscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Susan L. Sullivan,
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5', mRNA sequence.
B0950224
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                                                                                                                                  Conservative
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/lab_host="0H10B (phage resistant)"
/lab_host="0H10B (phage resistant)"
/note="0rgan: olfactory epithelium; Vector:
pcMV-SPORT6.1.ccdb; Site_1: EcoRV; Site_2: NotI; Cloned
unidirectionally. Primer: Oligo dT. Average insert size
2.2 kb .Constructed by ResGen, Invitrogen Corp. Note: this a NIH_MGC Library."
15 a NIH_MGC Library."
269 c 190 g 274 t 2 others
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/clone="IMAGE:6311019"
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95.1%;
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Mus musculus cDNA clone IMAGE:6311019
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                                                                                                                                                                                                                                        BQ018619 712 bp mRNA linear UI-H-DH1-awu-1-06-0-UI.s1 NCI_CGAP_DH1 Homo sapiens IMAGE:5823821 3', mRNA sequence.
BQ018619 BQ018619 BQ018619.1 GI:19753896
                                                                                                      Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
         cDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be found through the I.M. A.G. E. Consortium/LLNL at: http://image.llnl.gov
                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
                                                                                                                                             Mammalia; Eutheria; Primates; Catarrhini; Hominid
1 (bases 1 to 712)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence tag for this library is AGATCATTGC.
TAG_LIB-UI-H-DH1
TAG_TISSUE-Lung
TAG_SEC-AGATCATTGC"
a 163 c 192 g 181 t 2 others
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/clone_lib="NCI_CGAP_DH1"
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/db_xref="taxon:9606"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Unpublished (1999)
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602347846F1 NIH_MGC_90 Homo sapiens
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/lab_host="DBHOB (phage=resistant)"
/note="Organ: liver; Vector: pCwV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NHH_MGC Library."
a 236 c 209 g 207 t 1 others
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Plate: LLCM1869 row: e column: 18
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Tissue Procurement: ATCC
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Contact: Robert Strausberg,
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/db_xref="taxon:9606"
/clone="IMAGE:5258105"
/clone_lib="NIH_MGC_42"
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/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: poTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. | "
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## RESULT 1 Q96QU 10 Q96Q AC Q96Q AC Q96Q DT 01-D DT 01-D DT 01-D DT 01-C DE CUB GN CDUB Query Match Best Local S Matches 836 MEDLINE=21333000, Scherl-Mostageer M., Sommergruber m., Ambros P., Schweifer N.; "Identification of a novel gene, CDCP1, ov colorectal cancer."; Concogene 20:4402-4408(2001). R EMBL; AY026461; AAK02058.1; -REMBL; AY026461; AAK02058.1; -R EMBL; AY026461; AX026461; AAK02058.1; -R EMBL; AY026461; AX026461; 96QU7 PRELIMINARY; PRT; 836 AA. 096QU7; 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) CUB domain containing protein 1. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; SEQUENCE FROM N.A. CDCP1. NCBI\_TaxID=9606; 61 61 1 MAGLNCGVSTALLGVLLLGAARLPRGAEAFETALPRESNITVLIKLGTPTLLAKPCYIVI 60 SKRHITMLSIKSGERIVFTFSCQSPENHFVIEIQKNIDCMSGPCPFGEVQLQPSTSLLPT 120 SKRHITMLSIKSGERIVFTFSCQSPENHFVIEIQKNIDCMSGPCPFGEVQLQPSTSLLPT MAGLNCGVSIALLGVLLLGAARLPRGAEAFEIALPRESNITVLIKLGTPTLLAKPCYIVI 836; Similarity 100.0%; ilarity 100.0%; Conservative 0; Score 4394; Pred. No. 0; 0; Mismatches Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. FB4D2DBBDD35C519 CRC64; Abseher R., Hauptmann R., overexpressed in human DB 4; 0; Length Indels 0, Gaps 60 120

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HOMO SEPIENS (HUMBAN),
Eukaryota; Metazos;
Mammalia; Eutheria;
MCBI_TaxID=9606;
                                                                                                    SEQUENCE FROM N.A.

Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashi Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka Nakamura Y., Isogai T., Sugano S.;

"NEDO human cDNA sequencing project.";

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ database;

EMBL; AKO26622; BAB15511.1; -.

SEQUENCE 836 AA; 92874 MW; 9B980475C3E5C4C8 CRC64;
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RESULT 3

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PRELIMINARY; PRT; 649 AA.
AC Q9H8C2;
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DE CDNA FLJ13772 fis, clone PLACE4000300.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebi
OC Mammalia; Butheria; Primates; Catarrhini; Homir
OX NCBI_TaxID-9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PLACENTA;
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S., Takahashi-Fujii
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SEQUENCE FROM N.A.
Kawabata A., Hikiji
Okitani R., Ota T.,
                                                                                                           Homo sapiens (Human
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                       09H676 PRELIMINARY; PRT; 392 AA. 09H676; 01-MAR-2001 (TrEMBLrel. 16, Created) 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) CDNA: FLJ22534 fis, clone HRC13020 (Fragment).
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EMBL; AK023834; BAB14695.1; -

EMBL; AK023834; BAB14695.1; -
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Suzuki Y., Obayashi M., N
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EMBL; BC02
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01-MAR-2002 (TrEMBLrel. 20, Last sequence up
01-MAR-2002 (TrEMBLrel. 20, Last annotation
01-MAR-2002 (TrEMBLrel. 20, Last annotation
similar to hypothetical protein FLJ22969.
Homo sapiens (Human)
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Submitted (AUG-2000) to the EMBL/GenBank/DDBJ
EMBL; AKO26187; BAB15388.1; -.
NON_TER 392 392
SEQUENCE 392 AA; 44031 MW; 3E21C8B2703E52F
                                                                                                                                                                                                Hypothetical protein. SEQUENCE 343 AA; 3
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                TISSUE-KIDNEY;
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MAGLNCGVSIALLGVLLLGAARLPRGAEAFEIALPRESNITVLIKLGTPTLLAKPCYIVI
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BC021099; AAH21099.1; -
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99.78;
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                                                                                                                     Score 1779; DB 4; Length Pred. No. 3.1e-149;
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Pred. No. 6.4e-173;
1; Mismatches 0;
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                                                                                                Mismatches
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Q9-DEC-2001 (TrEMBLrel. 19, Createo)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUL-2001) to the EMBL; BC011340; AAH11340.1; MGD: MGI:2142933; AA409659.
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Mammalia; Eutheria;
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358
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HPNKGEIGVRETDIPLLHTQGPVETEE
                    HPNNGDVSSKDTDIPLLNTQEPMEPAE
                                           SGGSFIQPEVDTYRPPQGPMGDCPPTPPPLFSRTPTAKFTAEELAPSSPPESESEPYTFS
                                                       SSGSFLQPEVDTYRPFQGTMGVCPPSPPTICSRAPTAKLATEEPPPRSPPESESEPYTFS
                                                                                         FV-KKKKKVDKGPAVGIYNGNVNTQMP-QTQKFPKGRKDNDSHVYAVIEDTMVYGHLLQD
                                                                                                     CVKKKKKTINKGPAVGIYNGNINTEMPRQPKKFQKGRKDNDSHVYAVIEDTMVYGHLLQD
                                                                                                                                    SLTSVSWNISVPRDQVACLTFFKERSGVVCQTGRAFMIIQEQRTRAEEIFSLDEDVLPKP
                                                                                                                                                                                                                                  KQNSSVTLRAYAPSFQQEVSKQGLIVSYTPYFKEEGIFTVTPDTKNKVYLRSPNWDRGLP
                                                                                                                                                                                                                                                       KQNISVTLRTFAPSFQQEASRQGLTVSFIPYFKEEGVFTVTPDTKSKVYLRTPNWDRGLP
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Rodentia;
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Pred. No. 8.8e-J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; I
Sciurognathi; Muridae;
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-133;
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SMARR; SM00032; CCF; 2.
SMARR; SM00032; CCB; 2.
SMARR; SM000179; EGF_CA; 1.
SMARR; SM00020; TryP_SPC; 1.
SMARR; SM00020; TryP_SPC; 1.
PROSITE; PS001010; ASX_HYDROXYL; 1
PROSITE; PS01180; CUB; 2.
PROSITE; PS01180; CUB; 2.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_HIS; UNI
PROSITE; PS00135; TRYPSIN_SER; 1.
EGF=11ke domain; Glycoprotein; Hy
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(Ji X.) Azumi K., Sasaki M., Nonaka M.;
"Afficient origin of the complement lectin pathway revealed
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-1- SIMILARITY: CONTAINS 2 CUB DOMA(NS.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SIMILARITY: BELONGS TO PEPTIDASE FAMILY SIMILARITY: BELONGS TO PEPTIDASE FAMILY SIMILARITY: BELONGS TO PEPTIDASE FAMILY SIMILARITY: BELONGS TO PEPTIDASE FAMILY SIMILARITY: BELONGS TO PEPTIDASE FAMILY SIMILARITY: BELONGS TO PEPTIDASE FAMILY SIMILARITY: BELONGS TO PEPTIDASE FAMILY SIMILARITY: BELONGS TO PEPTIDASE FAMILY SIMILARITY: BELONGS TO PEPTIDASE FAMILY SIMILARITY: BELONGS TO PEPTIDASE FAMILY SIMILARITY: BELONGS TO PEPTIDASE FAMILY SIMILARITY: BELONGS TO PEPTIDASE FAMILY SIMILARITY: BELONGS TO PEPTIDASE FAMILY SIMILARITY: BELONGS TO PEPTIDASE FAMILY SIMILARITY: BELONGS TO PEPTIDASE FAMILY SIMILARITY: BELONGS TO PEPTIDASE FAMILY SIMILARITY: BELONGS TO PEPTIDASE FAMILY SIMILARITY SIMILARITY: BELONGS TO PEPTIDASE FAMILY SIMILARITY SIMILARITY: BELONGS TO PEPTIDASE FAMILY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARIT
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Eukaryota; Metazoa; Chordata; Urochordata;
Stolidobranchia; Pyuridae; Halocynthia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00084; sushi; 1. Pfam; PF00089; trypsin; 1.
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01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                  LLYCNSVF----SAELLTAHFGNFSSPNYPRSYPDNSNLTWNIRVQHGYRMSIRFSTFDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LCIIESVFEGEGSATLMSA-----NYPEGFPEDELMTWQFVVPAHLRASVSFLNFNL 271
                                                                                                                                                                                                                                 ----SKFIYTSQNEVRVTFVSDYSISLSGFQAHYAQIDINECELMETKKRTIIEDWD 161
                                                                                                                                                                                                                                                                           GILRLQFQVLVQHPQNESNKIYVVDLS-----NERAMSLTIEPRPVKQSRK------
    SFSYLVASAIPSQDLYFGSFCPGG------SIKQIQVKQNISVTLRTFAPSFQQ----
                                               SGHISSPEYP-----ELYAKLTDCSWTIQLREGLSVNLIFERAFGIEEHEEE----GC
                                                                                  HRYCQRKSYSLQVPSDILHLPVELHDFSWKLLVPKD-RLSLVLVPAQKLQQHTHEKPCNT
                                                                                                                                         ELVVCSHYCRNVPGSYYC----GCRPKFTLDANRHTCVASFCEN---
                                                                                                                                                                               -----FVPGCFVCLESRTCSSNLTLTSGSKHKISFLCDDLTRLWMNVEKTISCTD
                                                                                                                                                                                                                                                                                                                                                                     -----SNCERKEERVEYYIPGSTTNPEVFKLEDKQPGNMAGNFNLSLQGCDQDAQSP 323
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IPR000859;
IPR001881;
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Chymotrypsin
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EGF_Ca.
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Pred. No. 0.0029;
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Best Local S
Matches 100
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SMART; SM00042; CUB; 2.
SMART; SM000179; EGF_CA; 1.
SMART; SM00020; Tryp_SPc; 1.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Mannose-binding lectin-associated serine protease.
Triakis scyllium (Leopard shark) (Triakis scyllia).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes; Triakid
                                                                                                                  PROSITE; PSO0100, ASX, HYDROXYL; UNKNOWN_1.

PROSITE; PS01180; CUB; 2.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS00290; IG_MFC; UNKNOWN_1.

PROSITE; PS00240; TRYPSIN_DOM; 1.

PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.

Calclum-binding; EGF-11ke domain; Glycoprotein;
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InterPro;
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EMBL; AB009074; BAA86867.1; -.
HSSP; P00736; 1APQ.
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-I- SIMILARITY: CONTAINS 2 CUB DOMAINS.
-I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00722;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Two lineages of mannose binding lectin-associated (MASP) in vertebrates.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-99008558; PubMed-9794427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=30494;
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    Local Similarity
les 100; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                       PF00089; trypsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WSHSAPICQIKSCGVPQFLLDLPNSHIVEYENSKTTYSEVLDVTCNQWYGMISGASKWIC
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                                                                                                                                                                                                                                                                                                                                                                                                             PF00084; sush1; 2.
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                                                                                   Repeat; Serine protease 719 AA; 80425 MW; 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR003006; Ig_MHC.
IPR001254; Ser_protease_Try.
IPR000436; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR001314; Chymotrypsin. IPR000859; CUB_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR000152; Asx_hydroxyl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR001881
    Conservative
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                                                                                                                                                                                                                                                                                                                                                                   CHYMOTRYPSIN
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                      3.1%;
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    62;
                      Score 137.5; DB 13; Pred. No. 0.0045;
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  149;
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Gaps
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  SMART;
                                                                                                                                                            InterPro;
InterPro;
                                                                              Pfam; PF00431; CUB; Pfam; PF00008; EGF;
                                                                                                                                                                                                                                                                    -i- SIMILARITY: CONTAINS 26
EMBL; AF022247; AAC71661.1;
HSSP; P00740; 1EDM.
                                                                                                                                                                                                                                                                                                                                               antibodies is a megalin-binding peripheral homology to developmental proteins.";
J. Biol. Chem. 273:5235-5242(1998).
                                                                                                                                                                                                                                                                                                                                                                                                       "The intrinsic factor-vitamin B12 receptor and targe antibodies is a megalin-binding peripheral membrane
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MOESTINE S.K., KOZYTAKİ R., Kristlansen M.,
Rasmussen H.H., Brault D., Pontillon F., Goo
Hammond T.G., Verroust P.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                       SMART;
                                                                                                                                      InterPro;
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                                                                                                                                                                                                                                             InterPro;
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SM00042;
SM00179;
SM00001;
                                                                                                                                IPR000561;
IPR000742;
IPR001881;
                                                                                                                                                                                                                                  IPR000152; Asx_hydroxyl
                                                                                                                                                                                                                 IPR000859; CUB_domain
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EGF_2.
                                                                                                                                EGF_Ca.
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Sciurognathi; Muridae;
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ja F.O., Chri
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RESULT
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SIGNAL
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PROSITE; PS01180; CUB; 27.

PROSITE; PS00022; EGF_1; UNKNOWN_4.

PROSITE; PS01186; EGF_2; 2.

PROSITE; PS01187; EGF_CA; 4.

Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation;

Receptor; Repeat; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                 TAPLVIPYPQVWIHFVSNERVEYTGFYIEYSFTDCGGIRTGDNGVISSPNYPNLYSAWTH
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                                          VTICGSETLRPLTVDGPVLL
                                                                    LDLLFSVTLTPRTVDLTVIL
                                                                                                 PKQYDNNMNCTYLIDADPQSLVILTFVSFHLEDRSAITGTCDHDGLHI-IKGRNLSSTPL
                                                                                                                                                       TLLATSCGDVAPSPIVTSGNIFTAVFQSEEMAAQGFSASFISRCGRTFNTSPGDIISPNF
                                                                                                                                                                                  -----VVCQTGRAFMIIQEQRTRAEEIFS-----
                                                                                                                                                                                                             KSPHWPQTFPENSRCSWTVITHESKHWEISFDSNFRIPSSDSQCQNSFVKVWEGRLMINK
                                                                                                                                                                                                                                       RTPNWDRGLPSLTSVSW-------NISVPRDQVACL-TFFKERSG-----
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3623 AA;
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Conservative
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Pred. No. 0.054;
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InterPro; IPR001412; trNA-synt_I.
Pfam; PF00431; CUB; 7.
SMART; SM00042; CUB; 6.
PROSITE; PS00178; AA_TRNA_LIGASE_I; UN
PROSITE; PS01180; CUB; 7.
NON_TER
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Q96PQ1;
01-DEC-2001
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J. Biol. Chem. 0:0-0(2000).
-!- SIMILARITY: CONTAINS 6 CUB
EMBL, AF197159; AAF61487.1; -.
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Hammad S.M., Barth J.L., Knaak
"Megalin acts in concert with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cubilin (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                        ---EYYIPGSTTN-----PEVFKLEDKQPGNMAGNFNLSLQGCDQDAQSPGI
                                                                                                         SWNISVPRDQVACLTF
                                                                                                                                  DSSQTARGWKVSFRETIGPQQGCGGYLTEDSKSFVSPDHDSDGL---
                                                                                                                                                        EASR--QGLTVSFIP-----
                                                                                                                                                                               ----HD-----YLEVFDGPSIGNRSIGKFC
                                                                                                                                                                                                                                                                         NLSSTPLYTICGSETLRPLTIDGPVMLNFYSDAYITDFGFKISYRVANCGGIYSGTYGVL
                                                                                                                                                                                                                                                                                                LRLQFQVLVQHPQNESNKIYVVDLSNERAMSLT - - - - - IEPRPVKQSRKFVPGCFVCLES
                                                                                                                                                                                                                                                                                                                                                                 ETNDALLATSCGNVAPSPIVTLGNIFTAVFQSEEMPAQGFSASF-ISRCGRTFNSSTGDI
                                                                                    -WYIIAPENKLVKLTF
                                                                                                                                                                                                    QQHTHEKPCNTSFSYLVASAIPS-QDLYFGSFCPGGSIKQIQVKQNISVTLRTFAPSFQQ
                                                                                                                                                                                                                            NSPSFSYTNYPNNVYC----VYSLQVRNDRLIL-LRFNDFE----IVPSNLCS------
                                                                                                                                                                                                                                                -EKTISCTDHR----YCQRKSYSLQVPSDILHLPVELHDFSWKLLVPKDRLSLVLVPAQKL
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94; Conserv
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                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 127; DB
Pred. No. 0.04
62; Mismatches
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Last annotation updat
    Created)
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                                                                                                                                                        -YFKEEGVETVTPDTKSKVYLRTPNWDRGLPSLTSV
                           PRT;
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 4.
SMART; SM00406; IGv; 2.
SEQUENCE 595 AA; 64984 MW
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"A second uniquely human mutation affecting
J. Biol. Chem. 276:40282-40287(2001).
EMBL; AF282256; AAK71521.1; -.
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Mammalia; Eutheria;
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letazoa; Chordata;
ltheria; Primates;
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Last annotation updat
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson i.
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM ...:
STRAIN-BRISTOL N2;
Dante M., Wamsley P.;
The sequence of C. elegans
"The sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C45G7.5.
Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Eukaryota; Metazoa; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         076355

076355;

01-NOV-1998 (TrEMBLrel. 08,

01-NOV-1998 (TrEMBLrel. 17,

01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAY-1998) to the EMBL/GenBank/DDBJ EMBL; AF067611; AAC19183.1; TITCH TERROLZ126; Cadherin. PROSITE: PS50268; CADHERIN_2; 2. 80729ECDE64D9F SEQUENCE 986 AA; 109455 MW; 80729ECDE64D9F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BRISTOL N2;
MEDLINE-94150718; PubMed-7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhabditidae; Pel
NCBI_TaxID=6239;
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     642
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     NLDTSEVFFDANSKNFKRVKVEFVGD-----
                                                     TC-SSNLTLTSGSKH----KISFLCDDLTRLWMNVEKTISCTDHRYCQRKSYSLQVPSDI
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                                                                                                                                                               GI-LRLQFQVLVQHPQ-NESNKIYVVDLSNERAMSLTIEPRPVKQSRKFVPGCFVCLESR
                                                                                                                                                                                                                      RVENLDDNEPEFLPSALPIFQVPKNTSKPTAIGRLTARDADFSPIFYHLLPNCGTPESSD
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                                                                                                            NFNIDAEFGEIVYEPKVDPSSKMTEAEV---
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18.3%; Pred. No. 0.
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EMBL/GenBank/DDBJ databases
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Mismatches
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                                                                                                            Pfam; PF00431; CUB; 27.

R Pfam; PF00008; EGF; 6.

R SMART; SM00042; CUB; 26.

R SMART; SM00019; EGF_L1ke; 4.

R SMART; SM00010; EGF_L1ke; 4.

R PROSITE; PS001180; CUB; 27.

R PROSITE; PS01180; CUB; 27.

R PROSITE; PS01186; EGF_1; UNKNOWN_4.

PROSITE; PS01186; EGF_2; UNKNOWN_2.

R PROSITE; PS01187; EGF_L1ke domain; Glycoprotein; Hydroxylation; Rep Calcium-binding; EGF-11ke domain; Glycoprotein; Hydroxylation; Rep Calcium-binding; EGF-11ke domain; Glycoprotein; Hydroxylation; Rep Calcium-binding; EGF-11ke domain; Glycoprotein; Hydroxylation; Rep
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Best Local
                  Matches
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Q9TU53;
Q9TU53;
01-MAY-2000
01-MAY-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIINE-20021710; PubMed-10552972;
Xu D., Kozyraki R., Newman T.C., Fyfe J.C.;
"Genetic evidence of an accessory activity required specifically cubilin brush-border expression and intrinsic factor-cobalamin absorption.";
Blood 94:3604-3606(1999).
-I-SIMILARITY: CONTAINS 26 CUB DOMAINS.
EMBL; AF137066; AAF14258.1;
-HSSP; P35555; 1EMN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000859; CUB_domain.
InterPro; IPR000561; EGF-11ke.
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Local Local 154;
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                                            Similarity
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                  Conservative
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03VB7; 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) 01-MAR-2012 (TrEMBLrel. 20, Last annotation update) F0487H02.1 protein (OSJNBa0025P13.19 protein).

update)

Q93VB7

PRELIMINARY;

PRT;

724 ₿

Oryza sativa (Rice). Eukaryota; Viridiplantae; Str Spermatophyta; Magnoliophyta;

Streptophyta; Embryophyta; Trach yta; Liliopsida; Poales; Poaceae;

Tracheophyta;

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STRAIN-CV. NIPPONBARE;

STRAIN-CV. NIPPONBARE;

STRAIN-CV. NIPPONBARE;

Sasaki T., Matsumoto T., Yamamoto K.;

Sasaki T., Matsumoto T., Yamamoto K.;

Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, Bi
clone:OsJNBA0025Pl3:";

Clone:OsJNBA0025Pl3:";

SLMMItted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

REMBL; AP00288; BAB67842.1; -.

REMBL; AP002140; BAB5759.1; -.

REMBL; AP003140; BAB5759.1; -.

RINTERPRO; IPRO01525; CS_DNA_meth.

RROSITE; PS00094; CS_MTASE_1; UNKNOWN_1.

SEQUENCE 724 AA; 79780 MW; D6B3E09BEAF23253 CRC64;
Q9Y216 PRELIMINARY; PRT; 1406 AA.
Q9Y216; Q9N0E3;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UNOV-1999 (TrEMBLrel. 21, Last annotation update)
KIAAO980 protein (DJ691N24.1.1) (KIAAO980 protein, isoform
(Fragment).
KIAAO980 OR DJ691N24.1.
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Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto DNA, chromosome 1,
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
clone:P0487H02.";
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21.3%; Pred. No. 0.088;
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	ICCVKK 693	3GVLLLSALGLIICCVKK	SVTLTPRTVDLTVILIAAVGG	TSGKQLDLLFSVT	646	- Оу	
	IRREAE 762	ELHEKSQEVIWGLQEQLQDTARGPEPEQMGLAPCCTQALCGLALRHHSHLQQIRREAE	QEQLQDTARGPEPEQMGI	LEELHEKSQEVIWGL	703	Дb	
	ISNCSP 645	SFHHHSFWVNISNCSP		AEEIFSLDEDVL	615	VΩ	
	EGQKAD 702	ELMMEQVKEHYQDLRTQLETKVNYYERE IAALKRNFEKERKDMEQARRREVSVLEGQKAD	TQLETKVNYYERETAALE	ELMMEQVKEHYQDLR	643	дb	
	QEQRTR 614	TSVSWNISVPRDQVACLTFFKERSGVVCQTGRAFMIIQEQRTR	TSVSWNISVPRDQVACL-	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	572	Qy	
	PVSIET 642	-HSPSWSPDGRRRQLPGLGPAGISFLGNSAPVSIET	:	QAELEGLWARLPKNR-	593	Дb	
	571	RGLPSL	VSFIPYFKEEGVFTVTPDTKSKVYLRTPNWD	VSFIPYFKEEGVFTV	535	γo	
	DRNDEL 592	ERLALKL-QKDLEFVLKDKLEPQSAELLAQEERFAAVLKEYELKCRDLQDRNDEL	DLEFVLKDKLEPQSAELI	KLSDSERLALKL-QK	534	ДD	
	SRQGLT 534	-GSFCPGGSIKQIQVKQNISVTLRTFAPSFQQEAS	DLYFGSFCPGGSIKQI	NTSFSYLVASAIPSQDLYF-	477	Qy	
	IVEVVE 533	REKLTLALKENSRLQKEIVEVVE	LEWDVGRLQAEEAGL	EQAHRQRAA	487	рb	
	THEKPC 476	TD-HRYCQRKSYSLQVPSDILHLPVELHDFSWKLLVPKDRLSLVLVPAQKLQQHTHEKPC	VPSDILHLPVELHDFSW	TD-HRYCQRKSYSLQ	418	Qy	
	RSEVEAERELFW 486	-	ERAEKRNLEFVKEMDDCHSTLEQLTEKKIKHLEQGYRERLSLL-	ERAEKRNLEFVKEMD	432	Дb	
	EKTISC 417	PGCFVCLESRTCSSNLTLTSGSKHKISFLCDDLTRLWMNVEKTISC	GCFVCLESRTCSSNLTL	PRPVKQSRKFVP	361	Qy	
	KARQDL 431	SYQQGQVEQLARERDKARQDL	-ELTWALDNELMTVDSAVQQAALACYHQELSYQQGQ-	ELTWALDNELMT	382	, pp	
	MSLTIE 360	QPGNMAGNFNLSLQGCDQDAQSPGILRLQFQVLVQHPQNESNKIYVVDLSNERAMSLTIE	CDQDAQSPGILRLQFQVI	QPGNMAGNFNLSLQG	301	Qy	
	381	DEKVNLL	FPDQVLAMWTQEGIQNGREILQSLDFSV	FPDQVLAMWTQE	347	дь	
	FKLEDK 300	EGFPEDELMTWQFVVPAHLRASVSFLNFNLSNCERKEERVEYYIPGSTTNPEVFKLED	VPAHLRASVSFLNFNLS	PEGFPEDELMTWQFV	241	Qy	
	346	LLESSTRVKPSKAWSHYQVPEESGCHTTTTSSLVSLCSSLRLFSSIDDGSGFA-	HYQVPEESGCHTTTTSSI	LLESSTRVKPSKAWS	294	Дb	
	LMSANY 240	IKRLCIIESVFEGEGSATLMSANY	KMQEGVKMALHLPWFHPRNVSGFSIANRSSIKRLC	KMQEGVKMALHLPWF	187	Qy	
	: PAL 293	DGKVSLEEFQLGLFSHE	:	: :       :  :	250	Db	
	GTVSRI 186	ELQFSIPRLRQIGPGESCPDGVTHSISGRIDATVVRIGTFCSNGTVSRI	SIPRLRQIGPGESCPDG	KSIGL	133	Qу	
37	.406; 283; Gaps	DB 4; Length 1; 306; Indels	2.7%; Score 118.5; 17.8%; Pred. No. 0.61 tive 120; Mismatches	atch 2.7%; cal Similarity 17.8%; 154; Conservative 12	Query Match Best Local S Matches 154		
		A530020275943655 CRC64;	158951 MW; A5300	ENCE 1406 AA;	SEQUENCE	so	
			_HAND; UNKNOWN_1.	ITE; PS00018; EF	PROSITE;	DR:	
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		Kikuno R., Hirosawa M.,		<pre>MEDLINE=99246063; PubMed=10231032; Nagase T., Ishikawa K., Suyama M.,</pre>	MEDL Naga	RA RA	
				SEQUENCE FROM N.A. TISSUE-BRAIN;	TISS	RP	
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		Hominidae;		theria;	Mamm	<u></u>	
	stomi;	ertebrata; E	Chordata; Craniata; V	ryota; Metazoa;	Euka	88	
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DASQTQPRMWE	825 LLNTQEPMEPA 835	907 QDTEATQSPAPAPAPASHGPSERWSRWQPCGVDGDIVPKEPEPFGASAAGLEQPGARELP 966	789ATEEPPPRSPPESESEPYTFSHPNNGDVSSKDTDIP 824	862 -SGQEGTRGLLPLRPGCGERPLAWLAPGDGRESEEAAGAGPRRRQA 906	750 SSGSELQPEVDTYRPFQGTMGVCPPSPPTICSRAPTAKL 788	819 RAQMCVSLALEEEELELARGKRVDGPSLEAEMQALPKDGLVAG 861	694 KKKKTNKGPAVGIYNGNINTEMPRQPKKFQKGRKDNDSHYYAVIEDTMVYGHLLQD 749	1

Search completed: November 11, 2002, 11:35:52 Job tlme : 88 secs

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REFERENCE AUTHORS TITLE

Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Schweifer, N., Scherl-Mostageer, M., Sommergruber, W. and Abseher, R. Tumour-associated antigen (b345), characterised by an amino acid sequence as in seq. Id. No. 4

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                                              CTGTGGATGAATGTGGAAAAAACCATAAGCTGCACAGACCACCGGTACTGCCAAAGGAAA
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                                 GGGAACTTCAACCTCTCTGCAAGGCTGTGACCAAGATGCCCAAAGTCCAGGGATCCTC
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3781 GAATGAAAATCAAGGTGTCAGCAGAGCTGTGCTCCTTCTGAAGGCTCTAGGGAGAAGCCG 3840	CITAA	TACCAAACAGTGGCCCCCTGCATTAGTTTTCTGTTGCCACTGCAACCCATTACTTGGTAG	CTTTGACATTTAAAGAGAAATTTAGAGAATATTCTCATCCTCTAAAAATGTTTAAATATA 	CCTAG	3481 TAGGTCGGTTGTGGTTATCCCATTGTGGAAATTCATCTTGAATCCCATTGTCCTATAGT 3540 	3421 ATGTGTGTGTTTGAGCAGCATTGACACATATCTGCTTTGATAAGAGACTTCCTGATTCTC 3480	3361 AAACGTGTGCCTGTCCCCCAGGTGGTGGGAATAATTTACAATCTGTCCAACCAGAAAAGA 3420 	3301 GTAATAACTCATACTAACTGGTTTGGATGCCTGGGTTGTGACTTCTACTGACCGCTAGAT 3360 . 	TGGTC	CICIO	AGAGGCTTCCCCTCTTCAGGACAACAGTTCCAATTCCAAGGACCTACCT	AGAGAGGCCTGAGTCACCTAGCATAGGGTTGCAGCAGCCCTGGATTCAGAGTGTTAAAC	CATGACAGCTCATGTGCTCCTCAACTTAGGCTGTGCGGTTAGCCAGCC	TCAGTGGACTCATTCTAAGGCAAGACATTGAAAATGATGAATTCCAATCTGGATACAGT	GAGGAATTATACKGAAGGAACAGCAGGAGGTTTTCCTGGACACCGCCAACTTCACATTGC [	GTTTCATAAAGCAGGGCACTGAGACACCCGTCGGTGTTCCTAACCAGAAATCCTAAAGAA	ARCACICAGGAGCCCATGGAGCCAGCAGAATAACTTGATCCATTCCAGACGCTTTGCTGAAACACTCAGGAGGCCCATGGAGCCAGCAGAATAACTTGATCCATTCCAGACGCTTTGCTGAAACACTCAGGAGCCCATGGAGCCAGCAGAATAACTTGATCCATTCCAGACGCTTTGCTGAAACACTCAGGAGGCCATGGAGGCAGAAATAACTTGATCCATTCCAGACGCTTTGCTGAAACACTTGATCCAGAACGCTTTGCTGAAACACTTGATCCAGACGCTTTGCTGAAACACTTGATCCAGACGCTTTGCTGAAACACTTGATCCAGACGCTTTGCTGAAACACATAACATTGATCCAATACAAAAAAAA

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6000	ACTTGTCCCCTGGTTCAGTAGAGGCCCCGGTTTCCCCAGTTGTTGACTGTGACAGGCT	5941	Оу
5940	CTGTGCTTTAAATAAACAAATGTACCAAAAAACAAGTATCAAGCTGTTTAAGTGCTTCGG	5881	дь
5940	TGTGCTTTAAATAAACAAATGTACCAAAAAAAACAAGTATCAAGCTGTTTAAGTGCTTCG	5881	Оу
5880		8	дb
5880	CACTGGAAATAATTTATTCATTGCAGATACTTTTTAGGTGGCATTTTATTC	5821	Qy
5820	CAAGCCCACCGGACATGCCCTTGCTAAAGGTTAGCAGACTGGTGTGTGT	5761	Db
5820	AAGCCCACCGGACATGGCCTTGGTAAAGGTTAGCAGACTGGTGTGTGT	5761	Оу
5760	ATGCTGTGGTCATTGCACAGAAGGGAAAGGTCTCAAGGAAGAGTCAACTGGGACAAGCA	5701	дъ
5760	iggtcattgcacagaagggaaaggtctcaaggaagagtcaactgggac	5701	Qy
5700	GCTCATCCACGTGGTCTGCCATGCCTACGAGGAAGGCCAGCGCATGCAGGACTGGTCTCT	5641	Db
5700	ATCCACGTGGTCTGCCATGCCTACGAGGAAGGCCAGCGCATGCAGGACTGGTC	5641	Qy
5640	TCAGGGTCACTGGAAACAGTGAAGTGCCATTTGTTGAAGCCTACTGCATGCCAGCCCACT	5581	Db
5640	STCACTGGAAACAGTGAAGTGCCATTTGTTGAAGCCTACTGCATGCCAGCC	5581	Qy
5580	CAGCCTGAGGAACCCTGGCTCTTTTCTTTAAAGCCCAGGCCCACTTACATAAAACATT	5	DЪ
5580	CAGCCTGAGGAACCCTGGCTCTTTTCTTTAAAGCCCAGGCCCCACTTACATAAAAC	5521	· Qy
5520	TGGACAAGTTGCTGGCTCCTGAGACCAGTATTTCCTGGAGCTGTGCCTCAGTGAAGGGGC	5461	Db
5520	SACAAGTTGCTGGCTCCTGAGACCAGTATTTCCTGGAGCTGTGCCTCAGTGAAGGGG	5461	Qy
46		40	dd
5460	actgttgcctgcaaggacaccacgtggccattttccttcaactgagggctcaaa	5401	Ωу
5400		w	Db
5400	TTCCACCCAAGGTGGGATTGGCCTTCCTTAGGCTGGCTACTTGTCACCATCACC	5341	Оу
5340		28	Db
5340	CTCCATTCTCGACATTCCCCAACCTCCCAGCCCCTTCCAAGCAGGACTAGGTGCCCTG	N	Оу
5280	CTGCGGCTTCCTTCCCTCACTGAAGAGCCCTTATTTGAATTCACTGTGTGGAGCCCTAGC	5221	ф
5280	TGCGGCTTCCTTCCCTCACTGAAGAGCCCTTATTTGAATTCACTGTGTGGAGCCCTAG	5221	Оу
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5220	CAGTGACCCTTGGCCTTGTGAGCCGAGATGCTGACCCTGCATAAAGGGCCAAAGGAGG	5161	Qy
5160	TAAGTCATGCCCTTGGCGTTGCCTATGGCACCTTTCCCTTCTGAAAGTCTGGTTCCTGC	5101	Db
5160	AAGTCATGCCCTTGGCGTTGCCTATGGCACCTTTCCCCTTCTGAAAGTCTGGTTC	5101	Qy
5100	TAGTCTCCTAAATGGCGTGTACTGCAAGACCTCTTGAACACTTTCCAGAGGATAGGATAT	5041	Db
5100	AGTCTCCTAAATGGCGTGTACTGCAAGACCTCTTGAACACTTTCCAGAGGATAGGATA	5041	Оу
5040	ATTCACCTTGGAAATGCACCGCCTCAACTTGTTCACATGGCATAAATGAAAGGAATTTTA	4981	Db
5040	TTCACCTTGGAAATGCACCGCCTCAACTTGTTCACATGGCATAAATGAAAGGAATT	4981	Qy
4980	CAATATTTCTGCGGCAAAAACTTCCTTCAAAAAATAAATGTACTTCATTGTATTCAATGA	4921	DЬ
4980	AATATTTCTGCGGCAAAAACTTCCTTCAAAAAAATAAATGTACTTCATTGTATTCAA	4921	Оу

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Scherl-Mostageer,M., Sommerg
Ambros,P.F. and Schweifer,N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scherl-Mostageer,M., Sommergruber,W.,
Ambros,P. and Schwelfer,N.
Identification of a novel gene, CDCP1,
colorectal cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (31-JAN-2001) Exploratory Research, B Austria, Dr. Boehringergasse 5-11, Vienna 1121,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 5963)
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PCPFGEVQLOPSTSLLPTLNRFFIMDVKAHKSIGLELGFSIPRLRQIGPGESCPDGVT
HSISGRIDATVVRIGTFCSNGTVSRIKMGEGKVMALHLDWFHPRNVSGFSIANRSSIK
RLGIIESVFEGEGSATLMSANY PEGFPEDELMTWGFVVPAHLRASVSFLMFNLSNCER
REERVEYIPGSTTNPEVFKLEDKOPGNMAGNFNLSLQGCDQDAOSPGILRLQFQVLV
QHPQNESNKIYVVDLSBERAMSLTIEPRPVKOSRKFVPGCTVCLESRTCSSNLTLTSG
SKHKISFLCDDLTRLMMNVEKTISCTDHFRYCQRKSYSLQVPSDILHLPVELHDFSWKL
LVPKORLSLVLVPAQKLQQHTHEKPCNTSFSYLVASAIPSQDLYFGSFCPGGSIKQIQ
VKQNISVTLRTFAPSFQQEASRQGLTVSFIFYFKEEGVFTVTPDTKSKVYLRTPNWDR
GLPSLTSVSNNISVPROQVACLTFFKERSGVVCQTGRAWNIOCDGRTRAEEIFSLDED
VLPRVSFFHHISFWVMISNCSFTSGKOLDLLFSVTLTPRTVDLTVILIAVGGGVLLLS
ALGLIICCVKKKKKTNKGPAVGIYNGNINTEMPRQPKKFQKGRKDNDSHYYAVIEDT
MVYGHLLODSSGSFLOPEVDTYRPGCTMGVCPPSPTICSRAPTAKLATEEPPPRSP
PRESGEFENENGUNGGDKGVENGLTSVSNIS
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Location/Qualifiers
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83. .2593
                            PESESEPYTFSHPNNGDVSSKDTDIPLLNTQEPMEPAE'
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/protein_id="AAK02058.
/db_xref="GI:14328879"
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                                                                                                                                                                                                                                                                                                                                                                                         /chromosome="3"
                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                         translation-"MAGLNCGVSIALLGVLLLGAARLPRGAEAFEIALPRESNITVLI"
                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                        /note-"transmembrane
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2300	GCTCTTCTCGGTGACACTTACCCCAAGGACTGTGGACTTGACTGTCATCCTCATCGCAGC	24	Qy
2040	TCACAGCTTCTGGGTCAACATCTCTAACTGCAGCCCCACGAGCGGCAAGCAGCTAGACCT	96 8T	D Q
98	CCGGGCTGAGGAGCTTCAGCCTGGACGAGGATGTGCTCCCCAAGCCAAGCTTCCACCA	92	ф
2180	1 CCGGGCTGAGGAGATCTTCAGCCTGGACGAGGATGTGCTCCCCAAGCCAAGCCTTCCAACA	12	Qy
92		98	망
2120	CGGAGCGGCGTGGTCTGCCAGACAGGGCGCGCATTCATGATCATCCAGGAGCAGCGGA	90	δō
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1800	CAAGGTCTACCTGAGGACCCCCAACTGGGACCGGGGCCTGCCATCCCTCACCTC	7	망
2000		9	Qy
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9	ACGGTGTCCTTTATACCTTATTTCAAAGAGGAAGGCGTTTTCACGGTGACCCCTGACAC	88	δ
6		62	В
1880	TCGGTGACCCTTCGCACCTTTGCCCCCCAGCTTCCAACAAGAGGCCTCCAGGCAGG	82	δ
1620	GTACTTCGGCTCCTTCTGCCCGGGAGGCTCTATCAAGCAGATCCAGGTGAAGCAGAACAT 	156	B 8
5	CCCTGCAACACCAGCTTCAGCTACCTCGTGGCCAGTGCCATACCCAGCCAG	, ,	) Db
76	1 GAAGCCCTGCAACACCAGCTTCAGCTACCTCGTGGCCAGTGCCATACCCAGCCAG	7	ρ
1500	AAGGACAGGCTCAGCCTGGTGCTGCCAGCCCA	144:	рь
1700	GCTGGTGCCAGCCCAGAAGCTGCAGCAGCATACACACG	φ.	γQ
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1640	AGTGACATCCTCCACCTGCCTGTGGAGCTGCATGACTTCTCCTGGAAGCTGCTGGTGC	158	οy
38	AACCATAAGCTGCACAGACCACCGGTACTGCCAAAGGAAATCCTACTCCAGGTGCC	ω	문 5
л (	CATAAGCTGCACAGACCACGGTACTGCCAAAGGAAATCCTACTCACTC	5	Q Q
1520 1320	1 CAAACACAAAATCTCCTTTCCTTTGTGATGATCTGACACGTCTGTGGATGAATGTGGAAAA	146: 126:	B 6
1260	TGTTTCGTGTGTCTAGAATCTCGGACCTGCAGTAGCAACCTCACCCTGACATCTGGCT	120:	DЬ
1460	CTGTTTCGTGTGTGTCTAGAATCTCGGACCTGCAGTAGCAACCTCACCCTGACATCTGGCTC	4	δ
20		114:	р В
40	GCCATGTCACTCACCATCGAGCCACGGCCCGTCAAACAGAGCCGCAAGTTTGTCCCTG	w	ρ
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ω <b>4</b>	CAACATCCACAAAATGAAAGCAATAAAATCTACGTGGTTGACTTGAGTAATG&	N	Q Q
1080	CAAGGCTGTGACCAAGATGCCCAAGTTCTCAGGATCCTCCGGCTGCAGTTCCAAGTTTTT	102	B 5
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3	<b>ひまつましつ をそしかまし ひりじじじん そうじじん そうじじょうじゃ くじゅ そうをうじん ひじんしじん しゅうしょうしゅうしゅう しょうしゅうしゅう かんしゅう かんしゅう かんしゅう かんりょう かんりょう かんしゅう かんしゅう しゅう </b>	ر ا	긁

3380	ACTTCTACTGACCGCTAGATAAACGTGTGCCCTGTCCCCCA	3321	Qy
3180		3121	Db
3320	GATCAAATGTATAACCACCTAGCTCTTTTCACCTGACTTAGTAATAACTCATACTAACTG	3261	Qy
3120		3061	Db
3260	ATGAAAACGACAATGTGCCTTTTTATTATTATTTATTTGGTGGTCCTGTGTTATTTAAGA	3201	Qy
3060		3001	Db
3200	ACAACAGTTCCAATTCCAAGGAGCCTACCTGAGGTCCCTACTCTCACTGGGGTCCCCAGG	3141 2941	ДУ
3140	GCATAGGGTTGCAGCAAGCCCTGGATTCAGAGTGTTAAACAGAGGCTTGCCCTCTTCAGG	3081	Qу
2940		2881	
3080	TCAACTTAGGCTGTGCGGTTAGCCAGCCTGTAATGAGAGGAGAGAGGCCTGAGTCACCTA	3021 2821	Оу
3020 2820	GCAAGACATTGAAAATGATGAATTCCAATCTGGATACAGTCATGACAGCTCATGTGCTCC	7	Qy Db
2960	CAGCAGGAGGTTTTCCTGGACACCGCCAACTTCACATTGCTCAGTGGACTCATTCTAAGG	2901	Qy
2760		2701	Db
2900	GAGACACCCGTCCGTGTTCCTAACCAGAAATCCTAAAGAAGAGGAATTATACAGAAGGAA	28 <b>4</b> 1	Qy
2700		26 <b>4</b> 1	Db
2840	GCCAGCAGAATAACTTGATCCATTCCAGACGCTTTGCTGAGTTTCATAAAGCAGGGCACT	2781	Qy
2640		2581	Db
2780	TGGGGATGTAAGCAGCAAGGACACAGACATTCCCTTACTGAACACTCAGGAGCCCATGGA	2721	Qy
2580		2521	Db
2720 2520	ACCTCCTCGCTCCCCTGCTGAGTCTGAGAGTGAACCGTACACCTTCTCCCATCCCAACAA	0 4	Qy Db
2660	TCCCTCCCACCACCATATGCTCCAGGGCCCCAACTGCAAAGTTGGCCACTGAGGAGCC	2601	Qy
2460		2401	Db
2600	CTTCCTGCAGCCAGAGGT6GACACCTACCGGCCGTTCCAGGGCACCATGGGGGTCTGTCC	2541 2341	Оу
2540	GTATGCAGTCATCGAGGACACCATGGTATATGGGCATCTGCTACAGGATTCCAGCGGCTC	2481	Qy
2340		2281	Db
2480	TGAGATGCCGAGGCAGCCAAAAAAGTTTCAGAAAGGGCGAAAGGACAATGACTCCCCATGT	2421	Qy
2280		2221	Db
2420 2220	GAAGAAAAAGAAGACAAACAAGGGCCCCGCTGTGGGTATCTACAATGGCAACATCAATAC	2361 2161	Оу
2360	GGTGGGAGGTGGAGTCTTACTGCTGTCTGCCCTCGGGCTCATCATTTGCTGTGTGTG	2301	Qy
2160		2101	Db

4520	. TGTGTGCTCACATTACCCTTTTTTTTTTTTTTTTTTTTT	446	γo
4260	TGTAATGAAAAAGAAAGAACTGGGATTAATCTCTAATCAGGTGAGTAGACCATGAGACCAA	420	밁
4460	GTAATGAAAAAGAAAGACTGGGATTAATCTCTAATCAGGTGAGTAGACCATGAGACCAA	440:	ş
4200	CACAATGAGGCTAAGTGTTTGTTTCTACTGATCAATGCCCCTGCAGGTTGCATTTAT	4141	문
4400	CCCACAATGAGGCTAAGTGTTTGTTTCTACTGATCAATGCCCCTGCAGGTTGCATTTAT	4341	Qγ
4340 4140	GCCTTTAGAAGGGGTGTCCACTTCACCAGGTCACCACGCCCACACTACGCCCTATCACT	4281	₽ <b>%</b>
08	CCATGCTGGGGCTCACATTCTCACCTAGCAACAGCTGGCTG	02	, B
4280	GCCATGCTGGGGCTCACATTCTCACCTAGCAACAACTGGCTGG	22	Qy
4020	GGATGTTTTGTTTAGCTTGCGGACTCTAACACTTAAAAAAAA	396:	망
4220	GATGTTTTGTTTAGCTTGCGGACTCTAACACTTAAAAAAAA	416:	γQ
4160 3960	. TACCACACCTTCCTGCCACTGACTCCCACAGGAGAGGCTACAAAATGATCTGGCGCACAG	390:	p
3900	AACATAGCCACAGGTGGGGATTAGGACCAGGACATCTTTGGGGTGCTGTTATTCTGCC	- 60	B
4100	ACAACATAGCCACAGGTGGGGATTAGGACCAGGACATCTTTGGGGTGCTGTTATTCTGCC	2	γQ
3840	AGGATAATCTCTCCATCTAAAGATCCTTCATCATCCTGGAAGAGCCTTTTGCCATGCAAG	7	무 5
2	GGATAATCTCTCTATCTAAAGATCTTCTTCATCATCATCATCATCATCTTCATCAACGACGCCTTTTTTCATCAACGATCTTTTTTCATCAACGATCTTTTTTTT	۰ م	9
3980 3780	CACTGTGACACTGGCCCTCCCACTTCCCTCTTTGACTTACAAAGCCCACCAGGAAGATCC 	392	B 5
3720	CTAGAGGCTGCCTGCAGTCCAGTGGCTGGTCAAGCTTTTCTCACATGGCAT	σ	В
3920	TCACATGGCAT	386	80
		360:	밁
3860	CAGAGCTGTGCTCCTTCTGAAGGCTCTAGGGAGAAGCCGGTTCCTTGCCATTTCAAGCT	380:	γQ
3600	TTATAGTCCTGGGGATCAGAATTCCAAAATGGATGTCCCTGAATGAA	3541	В
3800	TTATAGTCCTGGGGATCAGAATTCCAAAATGGATGTCCCTGAATGAA	3741	Q
3740 3540	CATTAGTTTTCTGTTGCCACTGCAACCCATTACTTGGTAGCTTAAAAACAACACATTAGC	3681	р Q
3480	TTAGAGAATATTCTCATCCTCTAAAAATGTTTAAATATATACCAAACAGTGGCCCCCTG	342	문
3680	TTTAGAGAATATTCTCATCCTCTAAAAATGTTTAAATATATAT	3621	γQ
3420	CCTCAAGTTTCCATGTGCGGTTCTCCTAGCTGCAGCAATACTTTGACATTTAAAGAGAAA	336:	밁
3620	AAGTTTCCATGTGCGGTTCTCCTAGCTGCAGCAATACTTTGACATTTAAAGAGAAA	356	Qy
3360	CATTGTGGAAATTCATCTTGAATCCCATTGTCCTATAGTCCTAGCAATAAGAGAAATTT	330:	밁
3560	CATTGTGGAAATTCATCTTGAATCCCATTGTCCTATAGTCCTAGCAATAAGAGAAATTT	350:	Q
30	TTGACACATATCTGCTTTGATAAGAGACTTCCTGATTCTCTAGGTCGGTTCGTGGTTATC	24	망 .
5	TGACACATATCTGCTTTGATAAGAGACTTCCTGATTCTCTAGGTCGGTTCGTGGTTATC	4	Ş
2 4		18	당 .
3440	GGTGGTGGGAATAATTTACAATCTGTCCAACCAGAAAAGAATGTGTGTG	3381	γ

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TCTTTTCTTTAAAGCCCAGGCCCCACTTACATAAAACATTTCAGGGTCACTGGAAACAGT 5600	GAGACCAGTATTICCTGGAGCTGTGCCTCAGTGAAGGGGCCCAGCCTGAGGAACCCTGGC 5340	CACGTGGCCATTTTCCTTCAACTGAGGGCTCAAAACTCCTGGACAAGTTGCTGGCTCCT 528	CACGTGGCCATTTTCCCTTCAACTGAGGGCTCAAAACTCCTGGACAAGTTGCTGGCTC	11111 GGACA 522	GCCTTCCTTAGGCTGGCTACTTGTCACCCATCACCGACATCACTGTTGCCTGCAAGGACA 542	CAACCTCCCAGCCCTTCCAAGCAGGACTAGGTGCCCTGCATTCCACCCAAGGTGGGATT 5360 [	TGAAGAGCCCTTATTTGAATTCACTGTGTGGAGCCCTAGCCCTCCATTCTCGACATTCCC 5100	GAAGAGCCCTTATTTGAATTCACTGTGTGGAGCCCTAGCCCTCCATTCTCGACATTC	GAGCCGAGATGCTGACCCTGCATAAAGGGCCCAAAAGGAGGCTGCGGCTTCCCTTCCCTCAC 5040	AGCCGAGATGCTGACCCTGCATAAAGGGCCCAAAGGAGGGCTGCGGCTTCCCTTCCCTC	TGCCTATGGCACCTTTCCCTTCTGAAAGTCTGGTTCCTGCCCAGTGACCCTTGGCCTTGT 4980	ATGGCACCTTTCCCTTCTGAAAGTCTGGTTCCTGCCCAGT	ACTGCAAGACCTCTTGAACACTTTCCAGAGGATAGTATTTAAGTCATGCCCTTGGCGT 4920	CTGCAAGACCTCTTGAACACTTTCCAGAGGATAGGATATTTAAGTCATGCCCTTGG	 GTGT 486	CCTCAACTTGTTCACATGGCATAAATGAAAGGAATTTTATAGTCTCCTAAATGGCGTG	ი — 4-	TTCCTTCAAAAAATAAATGTACTTCATTGTATTCAATGAATTCACCTTGGAAATGCAC		GAGGGATTATGTTATAGCTTGTCAGCACAGTCCCAAGTTCAATATTTCTGCGGC		AATTACCTGCCCAGTAACTGTGGACTTTTGCTTCCTCACCCCTGCTCTGATCTGGAA	CCAAAGTGCTGGGATTACAGATGTGAGCCACGCATCCAGCCCCACACCTCATTTATAC 4840	CATGITGCCCAGGCTGGTCTCAACCTCCTGGGCTCAAGCAATCCTCCTGCCTCGGCCTC 456	76	TGGCACAACCACCATGCCCAGCTAATTTTGTATTTTTTTT	TCACTGGCACAAACCACCATGCCCAGCTAATTTTGTATTTTTTTGTAGAGACAGGGTTTCA 4700	GCAACCTCTGCCTCCTGGGCTCAAGCAATTCTCCCCACCTCAGCCTCCCAAATAGCTGGGA 4440	CAACCTCTGCCTCCTGGGCTCAAGCAATTCTCCCCACCTCAGCCTCCCAAATAGCTC	TGAGACAGGATCTCATTCTGTTGCCTAGGCTGGAGTGCAGTGCCGCAATCTCGGCTCACT 4380	GIGIGCICACATTACCCTITTCTTTTTTCTTTTTCTTTTTCTTTTTTTT

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REFERENCE
AUTHORS
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TGGAGTCTCGCCAAAAAAAAAAA 5963
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Sequence 1 from 1
AX353603
AX353603.1 GI:1
                                                                                                                                                                  Tumour-associated antigen (b345), characterised sequence as in seq. Id. No. 4 Patent: WO 0204508-A 1 17-JAN-2002;
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Mammalia; E
                                                                                                                                                                                                                                                  sapiens
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FEGEGSGATLMSANYPEGFPEDELMTWQFVVPAHLRASVSFLNFNLSNCERKEERVEYY
                                                                                              /organism="Homo sapiens"
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1. .214
215. .2464
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1. .5897
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Primates;
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GTCCCGGATCAAGATGCAAGAAGGAGTGAAAATGGCCTTACACCTCCCATGGTTCCACCC
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                                                        CTTCCCTGAGGATGAGCTCATGACGTGGCAGTTTGTCGTTCCTGCACACCTGCGGGCCAG
                                                                                                                                                  CAGAAATGTCTCCGGCTTCAGCATTGCAAACCGCTCATCTATAAAACGTCTGTGCATCAT
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                                             CTTCCCTGAGGATGAGCTCATGACGTGGCAGTTTGTCGTTCCTGCACACCTGCGGGCCAG
                                                                                                                                       CAGAAATGTCTCCGGCTTCAGCATTGCAAACCGCTCATCTATAAAACGTCTGTGCATCAT
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KIYVVDLSNERAMSLTIEDFRYVKQSKKEVPGCEVCLESSTCSSKLTLTSGSKHKISFL
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LRTFAPSFQQEASRQGLTVSFIPYFKEEGVFTVTDDTKSKVYLRTPNWDRGLPSLTSV
SWNISVERDQVACLTFFKERSGVVCQTGRAFWIIQEQRTRAEBIFSLDEDVLPKPSFH
HHSFWVNISNCSPTSKGLDLLFSVTLTPRTVDLTVILLAAVGGGVLLLSALGLIICC
VKKKKKTNKGPAVGIVNGNIYTEMPGSQKSFRKGERRWTPMCMQSSRFPWYMGICYR
IPAAPSCSQRWTPTGRSRAPWGSVLPPHPPYAPGDQLQSWPLRSHLLAPLLSLRVNRT
PSPIFTMGM"
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2210 1944	2151 GGATGTGCTCCCCAAGCCAAGCTTCCACCATCACAGCTTCTGGGTCAACATCTCTAACTG	р <b>о</b> у
2150 1884	2091 CGCATTCATGATCATCCAGGAGCAGCGGACCCGGGCTGAGGAGATCTTCAGCCTGGACGA	р <sub></sub> Оу
2090 1824	031 CCAGGTGGCCTGCCTGACTTTO	р <b>У</b>
2030 1764	1971 CTGGGACCGGGCCTGCCATCCCTCACCTCTGTGTCCTGGAACATCAGCGTGCCCAGAGA	pb Qy
1970 1704	1911 GGAAGGCGTTTTCACGGTGACCCCTGACACAAAAAGCAAGGTCTACCTGAGGACCCCCAA	g dy
1910 1644	1851 CTTCCAACAGAGGCCTCCAGGCAGGCTCTGACGGTGTCCTTTATACCTTATTTCAAAGA	p Q
1850 1584	1791 TATCAAGCAGATCCAGGTGAAGCAGAACATCTCGGTGACCCTTCGCACCTTTGCCCCCAG	рь
1790 1524	1731 CGTGGCCAGTGCCATACCCAGCCAGGACCTGTACTTCGGCTCCTTCTGCCCGGGAGGCTC	pb Qy
1730 1464	1671 AGCCCAGAAGCTGCAGCAGCATACACACGAGAAGCCCTGCAACACCAGCTTCAGCTACCT	р <b>2</b>
1670 1404	1611 GCATGACTTCTCCTGGAAGCTGCTGGTGCCCAAGGACAGGCTCAGCCTGGTGCTGCCCCTGGTGCTGCTGCTGCTGCTGCTGCT	рb
1610 1344	1551 CCAAAGGAAATCCTACTCACTCCAGGTGCCCAGTGACATCCTCCACCTGCCTG	p og
1550 1284	1491 TCTGACACGTCTGTGGATGAATGTGGAAAAAACCATAAGCTGCACAGACCACCGGTACTG	p Q
1490 1224	1431 CAGTAGCAACCTCACCCTGACATCTGGCTCCAAACACAAAATCTCCTTCCT	ру
1430 1164	1371 CGTCAAACAGAGCCGCAAGTTTGTCCCTGGCTGTTTTCGTGTGTCTAGAATCTCGGACCTG	Оу
1370 1104	1311 AATCTACGTGGTTGACTTGAGTAATGAGCGAGGCATGTCACTCAC	D Qy
1310 1044	1251 AGGGATCCTCCGGCTGCAGTTCCAAGTTTTGGTCCAACATCCACAAAATGAAAGCAATAA 	Db dy
1250 984	1191 GAACATGGCGGGGAACTTCAACCTCTCTCTCGCAAGGCTGTGACCAAGATGCCCAAAGTCC	Db Qq
1190 924	1131 CTACATCCCGGGCTCCACCACCACCCGAGGTGTTCAAGCTGGAGGACAAGCAGCCTGG	D 04

CTGTGTTATTTAAGAGATCAAATGTATAACCACCTAGCTCTTTTC 30	ATTTATTTGGTGGTC	96	DЬ	
CTGTGTTATTAAGAGATCAAATGTATAACCACCTAGCTCTT	TATTTGGTGG	323	Qy	
ACTGGGGTCCCCAGGATGAAAAACGACAATGTGCCTTTTTATTAT	4 GAGG	290	Db	
ACTGGGGTCCCCAGGATGAAAACGACAATGTGCCTTTTT	1 GAGGTCCCTACTCT	317	δĀ	
SCTTGCCCTCTTCAGGACAACAGTTCCAATTCCAAGGAGCCTACCT 31  - - - - - - - - - - - - - - - - - - -	1 AGTGTTAAACAGAGG	311 284	рь Оу	
CTGAGTCACCTAGCATAGGGTTGCAGCAAGCCCTGGATTCAG 2		78	문 5	
CTOACOTAGOATAGGGTTTGOAGOAAGCCCTGGATTCAG 3	1 таатсаса	<b>-</b>	Q i	
GTCATGACAGCTCATGTGCTCCTCAACTTAGGCTGTGCGGTTAGCCAGCC	1 TGGATACA	299 272	pb Qy	
ACTCATTCTAAGGGCAAGACATTGAAAATGATGAATTCCAA	4 TTCACAT	266	Db	
GGACTCATTCTAAGGGCAAGACATTGAAAATGATGAATTCCAATC 29	1 TTCACATTGCTCAGTGG	293	Qy	
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agaaggaacagcaggaggttttcctggacaccgccaa	1 TC	287	Qy	
ATAAAGCAGGGCACTGAGACACCCGTCCGTGTTCCTAACCAGAAA 28	1 GCTTTGCTGAGTTTCATA	281 254	dg VQ	
AGGAGCCCATGGAGCCAGCAGAATAACTTGATCCATTCCAGAC 2	4 TCCCTTAC	4	DЬ	
TCAGGAGCCCATGGAGCCAGCAGAATAACTTGATCCATTCCAGAC 28	1 TCCCTTACTGAACACTC	275	Qy	
CTCCCATCCCAACAATGGGGATGTAAGCAGCAAGGACACAGACAT 24	TGAACCGTACACCTTCTC	242	Db	
CCATCCCAACAATGGGGATGTAAGCAGCAAGGACACAGAC	GAAC	269	Qy	
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N	1 TGGGCATCT	51	Qy	
AATGACTCCCATGTGTATGCAGTCATCGAGGACACCATGGTAT	4 GAAAGGGCGAAAG	218	DЪ	
ACAATGACTCCCATGTGTATGCAGTCATCGAGGACACCATGGTATA 25	-	245	Qy	
CAACATCAATACTGAGATGCC - AGGCAGCCAAAAAAAGI	5 TGTGG	212	망	
GAACATCAATACTGAGATGCC	1 TGTGG	. 239	Qy	
CATTTGCTGTGAAAAAGAAGAAAAAGAAGACAAACAAGGGCCCCGC 21	5 CCTCGGGCTCATCA	206	Db	
STGTGAAAAAGAAGAAAAAAGAAGACAAACAAGGGCCCCCG	1 CCTCGGGCTCAT	233	Qγ	
TCATCCTCATCGCAGCGGTGGAGGTGGAGTCTTACTGCTGTCTGC 20	5 TGTGGACTTGACTG	200	Db	
ATCCTCATCGCAGCGGTGGGAGGTGGAGTCTTACTGCTGT	1 TGTGGACTTGACT	227	Qy	
CAAGCAGCTAGACCTGCTCTTCTCGGTGACACTTACCCCAAGGA	5 CAGCCCCACGAGCGG	194	Db	
CAAGCAGCTAGACCTGCTCTTCTCGGTGACACTTACCCCAAGG	AGCCCCACGAGC	221	Оу	

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4371 CTGATCAATGCCCCTGCAGGTTGCATTTATTGTAATGAAAAAGAAAG	4311 TCACCACAGCCCACACTACGCCCTATCACTTCCCACAATGAGGCTAAGTGTTTGTT	4251 AACAACTGGCTGGAGCTGGGCACCAGCTCTGCCTTTAGAAGGGGTGTCCACTTCACCAGG 4310	4191 ACTTAAAAAAAACCCCAGATCAGAAGATCTGGCCATGCTGGGGCTCACATTCTCACCTAGC 4250	4131 GGAGAGGCTACAAAATGATCTGGCGGACAGGGATGTTTTGTTTAGCTTGCGGACTCTAAC 4190	4071 AGGACATCTTTGGGGTGCTGTTATTCTGCCTACCACACCTTTCCTGCCACTGACTCCCACA 4130	4011 TCATCCTGGAAGAGCCTTTTGCCATGCAAGACAAACATAGCCACAGGTGGGGATTAGGACC 4070	3951 TTTGACTTACAAAGCCCACCACGAAGATCCAGGATAATCTCTCCATCTAAAGATCCTTCA 4010	3891 GTGGCTGGTCAAGCTTTTCTCACATGGCATCACTGTGACACTGGCCCTCCCACTTCCCTC 3950	3831 GGAGAAGCCGGTTCCTTGCCATTTCAAGCTTCTAGAGGCTGCTGCATTCCCAGGCTCCA 3890	3771 GGATGTCCCTGAATGAAAATCAAGGTGTCAGCAGAGCTGTGCTCCTTCTGAAGGCTCTAG 3830	TACTTGGTAGCTTAAAAACACACATTAGCTTATAGTCCTGGGGATCAGAATTCCAAAAT	3651 TTTAAATATATACCAAACAGTGGCCCCCTGCATTAGTTTTCTGTTGCCACTGCAACCCAT 3710	591 TGCAGCAATACTTTGACATTTAAAGAGAAATTTAGAGAATATTCTCATCCTCTAAAAATG	3531 GTCCTATAGTCCTAGCAATAAGAGAAATTTCCTCAAGTTTCCATGTGCGGTTCTCCTAGC 3590	3471 CCTGATTCTCTAGGTCGGTTCGTGGTGATCCCCATTGTGGAAATTCATCTTGAATCCCATT 3530	3411 CCAGAAAAGAATGTGTGTGTTTTGAGCAGCATTGACACATATCTGCTTTGATAAGAGACTT 3470 	3351 ACCGCTAGATAAACGTGTGCCTGTCCCCCAGGTGGTGGGAATAATTTACAATCTGTCCAA 3410	
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Submitted (33-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of
                                                      2 (bases 1 to 5573)
Isogai, T. and Otsuki, T.
Direct Submission
                                                                                                         Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Mishikawa,T., Nagai,K., Sugano,S., Takahashi-Fujii,A., Hara,H., Tahase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yanamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y. and Oshima,A. NEDO human cDNA sequencing project
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oligo capping; fis (full insert sequence).
Homo sapiens placenta cDNA to mRNA, clone_lib:PLACE4
clone:PLACE4000300.
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RLMMINTSTILTSGŠKHKISFLCDDLT
RLMMINTSTILTSGŠKHKISFLCDDLT
AOKLOOHTHEKPCNTSSYLVASAISHSODLTEGSTCPGGSIKOIQVKONISVTLRTFA
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TNPEYFKLEDKQPGNNAGNFNLSLQGCDQDAQSPGIIRLQFQVLVQHPQNESNKIYYV
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δλ Β δ	1109 GGAAGGAGGAGGGGTTGAATACTACATCCCGGGCTCCACCAACCCAACCCGAGGTGTTCA 1168	
₿ å	1229 GTGACCAAGATGCCCAAGGCCCAGGGATCCTCCGGCTGCAGTTCCAAGTTTTGGTCCAAC 1288	
B &	1289 ATCCACAAAATGAAAGCAATAAAATCTACGTGGTTGACTTGAGTAATGAGCGAGC	
₽ 6	1349 CACTCACCATCGAGCCAGGCCCGTCAAACAGAGCCGCAAGTTTGTCCCTGGCTGTTTCG 1408 	
B &	1409 TGTGTCTAGAATCTCGGACCTGCAGTAGCAACCTCACCCTGACATCTGGCTCCAAACACA 1468 	
ρ 9	1469 AAATCTCCTTCCTTTGTGATGATCTGACACGTCTGTGGATGAATGTGGAAAAAACCATAA 1528 	
B 5	1529 GCTGCACAGACCACCGGTACTGCCAAAGGAAATCCTACTCACTC	
g Q	1589 TCCTCCACCTGCCTGTGGAGCTGCATGACTTCTCCTGGAAGCTGCTGGTGCCCAAGGACA 1648	
β 6	1649 GGCTCAGCCTGGTGCTGGTGCCAGCCCAGAAGCTGCAGCAGCATACACACGAGAAGCCCT 1708 	
B 8	1709 GCAACACCAGCTTCAGCTACCTCGTGGCCAGTGCCATACCCAGCCAG	
β δ	1769 GCTCCTTCTGCCCGGGAGGCTCTATCAAGCAGATCCAGGTGAAGCAGAACATCTCGGTGA 1828 	
D Q	1829 CCCTTCGCACCTTTGCCCCCAGCTTCCAACAAGAGGCCTCCAGGCAGG	
B &	1889 CCTTTATACCTTATTTCAAAGAGGAAGGCGTTTTCACGGTGACCCCTGACACAAAAAGCA 1948 	
음 중	1949 AGGTCTACCTGAGGACCCCCAACTGGGACCGGGGCCTGCCATCCCTCACCTCTGTGTCCT 2008	
₽ 5	2009 GGAACATCAGCGTGCCCAGAGAGCCAGGTGGCCTGCCTGACTTTCTTT	
₽ \$	2069 GCGTGGTCTGCCAGACAGGGCGCGCATTCATGATCATCCAGGAGCAGCAGCAGCCGGGCTG 2128	
₽ ₹	2129 AGGAGATCTTCAGCCTGGACGAGGATGTGCTCCCCAAGCCAAGCTTCCACCATCACAGCT 2188	

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TATAACCACCTAGCTCTTTTCACCTGACTTAGTAATAACTCATACTAACTGGTTTGGAT 3	GACAATGTGCCTTTTATTATTATTATTTATTTGGTGGTGGTCTGTGTTATTTAAGAGATCAAAT 32 	TCCAATTCCAAGGAGCCTACCTGAGGTCCCTACTCTCACTGGGGTCCCCAGGATGAAAAC 26	CCAATTCCAAGGAGCCTACCTGAGGTCCCTACTCTCACTGGGGTCCCCAGGATC	TTGCAGCAAGCCCTGGATTCAGAGTGTTAAACAGAGGCTTGCCCTCTTCAGGACAACAGT 31	GCTGTGCGGTTAGCCAGCCTGTAATGAGAGGAGAGAGGCCCGAGTCACCTAGCATAGGG 25	CTGTGCGGTTAGCCAGCCTGTAATGAGAGGGAGAGAGGCCTGAGTCACCTAGCATAGG	N	gaaaatigatgaattccaatctggatacagtcatgacagctcatgtgctcctca <i>i</i>	GGTTTTCCTGGACACCGCCAACTTCACATTGCTCAGTGGACTCATTCTAAGGGCAAGACA 23	IGTTCCTAACCAGAAATCCTAAAGAAGGAAGTATTATACAGAAGGAACAGCAGGA 2		AATAACTTGATCCAGTCCCAGACGCTTTGCTGAGTTTCATAAAGCAGGGCACTGAGACACC 22	TAACTTGATCCATTCCAGACGCTTTGCTGAGTTTCATAAAGCAGGGCACTGAG	TAAGCAGCAAGGACACAGACATTCCCTTACTGAACACTCAGGAGCCCATGGAGCCAGCAG 22	AAGCAGCAAGGACACAGACATTCCCTTACTGAACACTCAGGAGCCCATGGAGCCAGCA	GCTCCCCTCCTGAGTCTGAGAGTGAACCGTACACCTTCTCCCATCACAACAATGGGGATG 21	C	CACCCACCATATGCTCCAGGGCCCCAACTGCAAAGTTGGCCACTGAGGAGCCACCTCCTC 26	AGCCAGAGGTGGACACCTACCGGCCGTTCCAGGGCACCATGGGGGTCTGTCCTCCCTC	GCCAGAGGTGGACACCTACCGGCCGTTCCAGGGCACCATGGGGGTCTGTCCTCCCTC	TCATCGAGGACACCATGGTATATGGGCATCTGCTACAGGATTCCAGCGGCTCCTTCCT	CATCGAGGACACCATGGTATATGGGCATCTGCTACAGGATTCCAGCGGCTCCTTC		GAGGCAGCCAAAAAAGTTTCAGAAAAGGGCGAAAGGACAATGACTCCCATGTGTATC	AGAAGACAAACAAGGGCCCCGCTGTGGGTATCTACAATGGCAACATCAATACTGAGATGC 18	GAAGACAAACAAGGGCCCCGCTGTGGGTATCTACAATGGCAACATCAATACTGAGATG	GTGGAGTCTTACTGCTGTCTGCCCTCGGGCTCATCATTTGCTGTGTGAAAAAGAAGAAAA 17	TGGAGTCTTACTGCTGTCTGCCCTCGGGCTCATCATTTGCTGTGTGAAAAAGAAGAAA	CGGTGACACTTACCCCAAGGACTGTGGACTTGACTGTCATCCTCATCGCAGCGGTGGGAG 17	GGTGACACTTACCCCAAGGACTGTGGACTTGACTGTCATCCTCATCGCAGCGGTGGGA	TCTGGGTCAACATCTCTAACTGCAGCCCCACGAGCGGCAAGCAGCTAGACCTGCTCTTCT 16	CTGGGTCAACATCTCTAACTGCAGCCCCACGAGCGGCAAGCAGCTAGACCTGCTCTTC

4169 TGTTTAGCTTGCGGACTCTAACACTT - AAAAAACCCCAGATCAGAAGATCTGGCCATGC 4227	3360 CACTGGCCCTCCCACTTCCCTCTTTTGCAAAAGCCCACCAGGAAGATCCAGGAACATA 3419 3989 CTCTCCATCTAAAGATCCTTCATCATCATCAGAAGACCACCAGGAAGATCCAGGAACATA 4048	CTGGGGATCAGAATTCCAAAATGGATGTCCCTGAATGAAAATCAAGGTGTCAGCAGAGCT	3509 GARATTCATCTTGAATCCCATTGTCCTATAGTCCTAGCAATAAGAAAATTCCTCAAGT 3568	2700 GTATAACCACCTAGCTCTTTTCACCTGACTAGTAATAACTCATACTAACTA
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                       Direct Submission
Submitted (10-JAN-2002) Genome Center, University
Box 352145, Seattle, WA 98195, USA
3 (bases 1 to 163115)
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A.,
Saenphimmachak, C., Phelps, K.A., Buckley, D.,
                                                                                                                                                                                                                                                                                                                 163115 bp DNA
Homo sapiens chromosome 3 clone RP11-578F5,
AC105902
                                                                                                                                                                              Mammalia; Eutheria; Primates; Catarrhini; Hc
1 (bases 1 to 163115)
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A.,
Saenphimmachak, C., Phelps, K.A., Buckley, D.,
                                                                                                           2 (bases 1 to 163115)
Kaul,R.K., Olson,M.V., Raymond,C.
                                                                                                                                          Unpublished
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Haugen, E.D.
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Primates;
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                                                                                                              Haugen, E
                                                                                   University
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Kibukawa, M., Raymond, C.
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JÓURNAL
Overlapping Sequences:
5': RP11-68104 (UWGC:bc0528) AC104165
3': RP11-487J21 AC010170, 50065-bp ov
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                                                                                                                                             Center project name: chr-3
Center clone name: RP11-578F5 (bc0477)
Center clone name: RP11-578F5 (bc0477)
Center clone name: RP11-578F5 (bc0477)

Sequencing vector: plasmid; 100% of reads
Chemistry: Dye-terminator ET; 29% of reads
Chemistry: Dye-terminator Big Dye; 71% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 163063 bases at least Q40
Consensus quality: 163110 bases at least Q30
Consensus quality: 163115 bases at least Q20
Insert size: 163115; sum-of-contigs
Quality coverage: 9.1x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.genome.washington.edu
Contact: uwgchtgs@u.washington.edu
Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: University of Washington Genome Center
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Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible f GenBank flat file format but are available as part of this entry's ASN.1 file. from zero

overlap

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mil subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:
This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies experimental and predicted values. Uniquely

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			111111		1111111
6921	6785	<800	512	789	740
2097	2067	6416	6382	<800	6
3352	3349	3097	3091	8823	8696
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II	BglII	III	HindIII	RI	EcoRI
		ed lines.	fragments are separated by dashed lines.	are separa	fragments

<b>-</b>	871 897 7321 797 789 5620 15170 15087 1720 919 897 3901 2182 2206 9970 214 <800 3602 6473 6579 522 1456 1431 4155 682 <800 3891 3675 3703 3267 3439 3449 50 10009 10022 4248 6068 6125 1035 11400 11202 3002
13421 1769 1804 2986 5507 5488 8119 144 <800 4507 1459 1448 2257 70 <800 <800 3690 3725 4507 102 <800 4819 1903 1951 1437 5124 5172 2083 367 <800 765 7100 7161 1310 5890 5897 3542 1814 1804 1661 125 <800 5065 117 <800 5065 117 <800 5065 1951 1661 4899 4924 1661 774 760 5065 10749 10446 2525 1620 1587	1202 18054 18054 2066 2066 3551 3798 7798 1844 11354 1354 1358 291 291 2935 2935 2935 2935 2935 2935
DATE COUNT 43894 & 36993 C 37715 9 44513 t  Query Match Bast Local Similarity 99.58; Pred. No. 0; Best Local Similarity 99.58; Pred. No. 0; Matches 3791; Conservative 0; Mismatches 17; Indels 1; Gaps 1;  Qy 2346 TTGCTTGTGAAAAAGAACAAAAAGGGCCCGCCTGGGGTATCTACAA 2405  Q1 2407 TTCCANTTTCCAAATAGGAAAAAGAACAAAAAGGGCCCGCCTGGGGTATCTACAA 2405  Qy 2406 TGGCAACATCAATAGGAAAAGAAGAAAAAAGGGCCCGAAAGGA 24465  Qy 2406 CAATGACCTCAATAGTGAAATGCCGAGGCAGCCAAAAAAGGTTCAGAAAGGACAAAGGA 24465  Qy 2406 CAATGACCTCCATCTGGAGTGCGGGCAGCCAAAAAAGGTTCAAAAGGACTACGAAAGGA 24462  Qy 2526 GGATTCCAGCGGCTCCTTCCTGCCGCGAGGAACACATGGTATATGGGCATCTGCGTACA 2402  Qy 2526 GGATTCCAGCGCTCCTTCCTGCAGCAGAGGTGGAAACCTACGGCCCAACTGCTACA 24042  Qy 2526 GGATTCCAGCGGCTCCTTCCTGCAGCAGAGGTGGAAACCTACGGGCCCAACTGCTACA 24042  Qy 2526 CATGGGGGTCTGTTCCTCCCCCCCCCCCCCCACCATATGCTCCAAGGGCCCAACTGCTACA 24042  Qy 2526 CATGGGGGCTCTTCTCCCCCCCCCCCCCCCCACCATATGCTCCAAGGGCCCCAACTGCTACA 2525  Qy 2526 GGATTCAGGGGCTCTTCTCCCCCCCCCCCCCCCCACCATATGCTCCAAGGGCCCCAACTGCTACATTT 2942  Qy 2526 CATGGGGGCTCTTCTCCCCCCCCCCCCCCCCCCCACCATATGCTCCAAGGGCCCCAACTGCAACTT 2992  Qy 2526 GGCCATGAGGAACCACTCCCTCCCCCCCCCCCCCCCACCATATGCTCCAAGGGCCCCAACTGCAACTT 2992  Qy 2526 TCAGGAGGCCACTGAGGACACACTGCTCCTCCCTCCCTCC	B892  1257  1257  10114  10114  10114  10115  Location/Qualifiers  1. 163115  /organism="Homo sapiens" /db_xref="taxon:9606" /db_xref="taxon:9606" /db_xref="RP11-578F5" /clone="RP11-578F5" /clone="RP11-578F5" /clone="TP715 or 44513

Ş	2946	GACTCATTCTAAGGGCAAGACATTGAAAATGATGAATTCCCAATCTGGATACAGTCATGA 30	05
ф	73621	GACTCATTCTAAGGGCAAGACATTGAAAATGATGCAATTCCAATCTGGATACAGTCATGA 73	562
g	3006	CAGCTCATGTGCTCCTCAACTTAGGCTGTGCGGTTAGCCAGCC	65
S	73561		502
β Q	3066 73501	GGCCTGAGTCACCTAGCATAGGGTTGCAGCAAGCCCTGGATTCAGAGTGTTAAACAGAGG 31:	25 442
g	3126	AGGAGCCTACCTGAGGTCCCTACTCTC 31	85
5	73441		382
ρ δ	3186 73381	TTATTTGGTGGTC 32             TTATTTGGTGGTC 73	45 322
4g	3246 73321	CTGTGTTATTAAGAGATCAAATGTATAACCACCTAGCTCTTTTCACCTGACTTAGTAAT 33	05 262
₽	3 <u>3</u> 06	AACTCATACTAACTGGTTTGGATGCCTGGGTTGTGACTTCTACTGACCGCTAGATAAACG 33	65
2	73261		202
g	3366	TGTGCCTGTCCCCCAGGTGGTGGGAATAATTTACAATCTGTCCAACCAGAAAAGAATGTG 34	25
V	73201		142
β	3426	TGTGTTTGAGCAGCATTGACACATATCTGCTTTGATAAGAGACTTCCTGATTCTCTAGGT 34:	85
δ	73141		082
99	3486	CGGTTCGTGGTTATCCCATTGTGGAAATTCATCTTGAATCCCATTGTCCTATAGTCCTAG 35.	45
99	73081		022
유	3546	CAATAAGAGAAATTTCCTCAAGTTTCCATGTGCGGTTCTCCTAGCTGCAGCAATACTTTG 36	05
안	73021		962
g	3606	ACATTTAAAGAGAAATTTAGAGAATATTCTCATCCTCTAAAAATGTTTAAATATATACCA 36	65
94	72961		902
β	3666	AACAGTGGCCCCCTGCATTAGTTTTCTGTTGCCACTGCAACCCATTACTTGGTAGCTTAA 37	25
δ	72901		842
ρ	3726	AAACAACACATTAGCTTATAGTCCTGGGGATCAGAATTCCAAAATGGATGTCCCTGAATG 37:	85
δ	72841		782
да	3786	AAAATCAAGGTGTCAGCAGAGCTGTGCTCCTTCTGAAGGCTCTAGGGAGAAGCCGGTTCC 38.	.45
<b>У</b> О	72781		722
d	3846	TTGCCATTTCAAGCTTCTAGAGGCTGGCTGCATTCCCAGGCTCCAGTGGCTGGTCAAGCT 39	05
Qy	72721		662
ρ	3906	TTTCTCACATGGCATCACTGTGACACTGGCCCTCCCCACTTCCCTCTTTGACTTACAAAGC 39.	65
δ	72661		602
β	3966	CCACCAGGAAGATCCAGGATAATCTCTCCATCTAAAGATCCTTCATCATCCTGGAAGAGC 40.	25
δ	72601		542

5164	GTCATGCCCTTGGCGTTGCCTATGGCACCTTTCCCTTCTGAAAGTCTGGTTCCTGCCCAG	5105	Qy
71462		.71521	מם
5104	TCCTAAATGGCGTGTACTGCAAGACCTCTTGAACACTTTCCAGAGGATAGGATATTTAA	5045	Qy
71522		71581	qa
5044	CCTTGGAAATGCACCGCCTCAACTTGTTCACATGGCATAAATGAAAGGAATTTTATAGT	4985	Оу
4984 71582	ATTTCTGCGGCAAAAACTTCCTTCAAAAAATAAATGTACTTCATTGTATTCAATGAATTC	4925 71641	Оу
16	GCTCTGATCTGGAAGGAGAGGGATTATGTTATAGCTTGTCAGCACAGTCCCAAGTTCAAT	70	Db .
N	тстсатстооддостатского в температельного по в предстателя в постород в постор в посто	486	Ş
7 0	ACACCCTCATTTATACCATTACCTGCCCAGTAACTGTGGACTTTTGCTTCCTCACCCCT	71761	B 2
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4804 71762	CTCCTGCCTCCGCAAAGTGCTGGGATTACAGATGTGAGCCACCGCATCCAGCCCC  [	4745 71821	p, Qy
71822	AGAGACAGGGTTTCACCATGTTGCCCAGGCTGGTCTCAACCTCCTGGGCTCAAGCAATC	71881	рь
4744	TAGAGACAGGGTTTCACCATGTTGCCCAGGCTGGTCTCAACCTCCTGGGCTCAAGCAATC	4685	. Qy
71882		9	Db
4684	CCCAAATAGCTGGGATCACTGGCACAAACCACCATGCCCAGCTAATTTTTGTATTTTTTG	4625	γQ
71942	GCAATCTCGGCTCACTGCAACCTCTGCCTCCTGGGCTCAAGCAATTCTCCCCACCTCAGCC	72001	Db
4624	CAATCTCGGCTCACTGCAACCTCTGCCTCCTGGGCTCAAGCAATTCTCCCCACCTCAGCC	4565	γQ
72002	CTTTTTTTTTAATGTGAGACAGGATCTCATTCTGTTGCCTAGGCTGGAGTGCAGTGGC	72061	Db
4564	TTTTTTTTTTAATGTGAGACAGGATCTCATTCTGTTGCCTAGGCTGGAGTGCAGTGGC	4505	Оу
72062		72121	ממ
4504	AGACCATGAGACCAATGTGTGCTCACATTACCCTTTTTCTTTTTTTT	4445	γQ
72122			Db
4444	GCAGGTTGCATTTATTGTAATGAAAAAGAAAGACTGGGATTAATCTCTAATCAGGTGAG	4385	Qy
72182	ACTACGCCCTATCACTTCCCACAATGAGGCTGAGTGTTTGTT	72241	Db
4384	TACGCCCTATCACTTCCCACAATGAGGCTAAGTGTTTGTT	4325	νδ
N		30	מַּם
4324	CTGGGCACCAGCTCTGCCTTTAGAAGGGGTGTCCACTTCACCAGGTCACCACAGCCCAC		O <sub>V</sub>
72302		72361	Db
4264	AGATCAGAAGATCTGGCCATGCTGGGGCTCACATTCTCACCTAGCAACAACTGGCTGG	4205	Qy
72362	TGGCGCACAGGGATGTTTGTTTAGCTTGCGGACTCTAACACTTAAAAAAAA	72421	ДĎ
4204	ATCTGGCGCACAGGGATGTTTTGTTTAGCTTGCGGACTCTAACACTT-AAAAAAACCC	4146	VΩ
72422	TGTTATTCTGCCTACCACCCTTCCTGCCACTGACTCCCACAGGAGAGGCTACAAAA	72481	Db
4145	GCTGTTATTCTGCCTACCACACCTTCCTGCCACTGACTCCCACAGGAGAGGCTACAAAA	4086	Qy
72482	CTTTTGCCATGCAAGACATAGCCACAGGTGGGGATTAGGACCAGAACATCTTTGGGG	72541	ДĎ
4085	TTTTGCCATGCAAGACAACATAGCCACAGGTGGGGATTAGGACCAGGACATCTTTGGGG	4026	Qy

do Qy	8 8	B 6	B 8	g 8	В <del>8</del>	В 8 8	g Q	р 5	g Q	g 8	å Ö	р 6	B 8	₿ <b>%</b>	₽ 5	р О	8
6125 70441	6065 70501	6005 70561	5945 70621	5885 70681	5825 70741	5765 70801	5705 70861	5645 70921	5585 70981	5525 71041	5465 71101	5405 71161	5345 71221	5285 71281	5225 71341	5165 71401	71461
ATAAAATAATAGTCTTGGAGTCTCGCCA 6153 	AAGTTCTTTCCTCTTCATTTGATGCCGTGCACTGTGTGAAGCAGATGTTTTTGTCCGGAA 6124 	TGGCCTCAGCAGATGCTGTCTTAATTTGTGGATACAGAAAAGCCAGGCTTTGGGATAC 6064 	TIGTCCCCTGGTTCAGTAGAGGCCCCGGTTTCCCAGTTGTTGACTGTGACAGGCTCAGCA 6004 	GCTTTAAATAAACAAATGTACCAAAAAACAAGTATCAAGCTGTTTAAGTGCTTCGGCTAC 5944 	CACTGGAAATAATTTATTCATTGCAGATACTTTTTAGGTGGCATTTTATTCATTTCCTGT 5884 	CCCACCGGACATGGCCTTGGTAAAGGTTAGCAGACTGGTGTGTGT	CTGTGGTCATTGCACAGAAGGGAAAGGTCTCAAGGAAGAGTCAACTGGGACAAGCACAAG 5764 	ATCCACGTGGTCTGCCATGCCTACGAGGAAGGCCAGCGCATGCAGGACTGGTCTCTAATG 5704 	GGTCACTGGAAACAGTGAAGTGCCATTTGTTGAAGCCTACTGCATGCCAGCCCACTGCTC 5644 	CCTGAGGAACCCTGGCTCTTTTCTTTAAAGCCCCAGGCCCCACTTACATAAAACATTTCAG 5584 	CAAGTTGCTGGCTCCTGAGACCAGTATTTCCTGGAGCTGTGCCTCAGTGAAGGGGCCCAG 5524 	GTTGCCTGCAAGGACACCACGTGGCCATTTTCCTTCAACTGAGGGCTCAAAACTCCTGGA 5464 	CACCCAAGGTGGGATTGGCCTTACGCTGACTACTTGTCACCATCACCGACATCACT 5404 	CATTCTCGACATTCCCCAACCTCCCAGCCCCTTCCAAGCAGGACTAGGTGCCCTGCATTC 5344 	GGCTTCCTTCCCTCACTGAAGAGCCCTTATTTGAATTCACTGTGTGGAGCCCTAGCCCTC 5284 	TGACCCTTGGCCTTGTGAGCCGAGATGCTGACCCTGCATAAAGGGCCAAAGGAGGGCTGC 5224 	

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                                                                                                                                                                                                                                                                Overlapping Sequences:
5': Rpl1-348pl0 (UWGC:bc0377) AC124045
3': Rpl1-578F5 (UWGC:bc0477) AC105902,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200956 bp DNA linear PRI 27-JUN Homo sapiens chromosome 3 clone RP11-68104, complete sequence. AC104165 AC068625 AC104165.2 GI:21617715
Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (27-JUN-2002) Genome Center, University of Washin Box 352145, Seattle, WA 98195, USA On Jun 27, 2002 this sequence version replaced gi:17352429.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (05-DEC-2001) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA 3 (bases 1 to 200956)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A.,
Saenphimmachak,C., Phelps,K.A., Buckley,D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota;
Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                          sequencing vector: unknown; 42% of reads sequencing vector: plasmid; 58% of reads chemistry: Dye-terminator ET; 80% of reads chemistry: Dye-terminator Big Dye; 20% of reads chemistry: Dye-terminator Big Dye; 20% of reads Assembly program: Phrap; version 0.990319 consensus quality: 200732 bases at least Q40 consensus quality: 200909 bases at least Q30 consensus quality: 200947 bases at least Q20 Insert size: 200956; sum-of-contigs quality coverage: 10.4x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project Information
Center project name: chr-3
Center clone name: RPI1-68104 (bc0528)
------ Summary Statistics
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Drafting Center: WUGSC
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                                                                                                                                                                                                                                                                        95352-bp overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rouse, G., Wu, Z.,
Kibukawa, M., Raymond, C.
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mil subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

10749     10616     1629     1629     2440     2446       1620     1602     7261     7427     1682     1662       8868     8810     7837     7939     1660     1662       5884     5889     3940     4106     4912     491       1521     1529     756     760     2470     2446       771     799     2395     2496     8892     8765       11706     11675     5310     5399     1257     1243	5028 3183 799 16952 1	1955 1919 3477 3529	; ;	1814 1816 1993 1932 2058 2110 125 <800 3153 3186 745 <800	5889 153 <800 1462	367 <800 645 <800 286 <800 7100 6934 1177 1170 4633 4784	5124 5028 12014 11879 4368 4477	1903 1919 8458 8571 45 <800	<800 1221 1170 4465	70 <800 4100 4106 2978 3031 3690 3725 779 760 8146 8133	1439 96 <800 5736	<800 11400 11207 449	6846 6934 6068 6154 512 <800	8 5288 8696 8571 3534	SeqDerMap FngrPrnt SeqDerMap FngrPrnt SeqDerMap FngrPrnt	re are no significant remaining discrepanci imental and predicted values. Uniquely orde arated by dashed lines.  ECORI  ECORI  HindII	The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC.  Small fragments below a variable cutoff (approximately 400-800 bp)	This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given helow
-		-		-							-	•				-		
Qy 2346 TTGCTGTGAAAACAAAACAAAACAAAACAAAACAAACCCCCCGCTGTGGGTATCTACAA 2405	Query Match Best Local Similarity 99.5%; Pred. Matches 3791; Conservative 0; Mis		317		1070 1069  4665 4675		207 <800  5047 5028	<800	1472 1439	6934	3825 3725		1 - 1 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2 -	5343 5288  6819 6934	49 5288	4 1 4	5177 52882916 2950	369 <800 2
;AAACAA          AAACAA                	3769.8 No. 0; matche							2905	1681 741	8568	2082	:	5394	8214  5836	3059	7411	4082 7866	21139
	Score 3769.8; DB 9; Length 200956; Pred. NO. 0; O; Mismatches 17; Indels 1; G	7228	2449	1023	4768  1083	1250	6129 1674	2905 3005	:	8568 8571	2082 2097 12931	419 <800	5394 5399 4817	8571 5849	3059 3186		4106 1 7939	1139 21498 10114

3665	Qy 3606 ACATTTAAAGAGAAATTTAGAGAATATTCTCATCCTCTAAAAATGTTTAAATATATAT
3605 178667	Qy 3546 CAATAAGAGAAATTTCCTCAAGTTTCCATGTGCGGTTCTCCTAGCTGCAGCAATACTTTG
3545 <sup>°</sup> 178727	QY 3486 CGGTTCGTGGTTATCCCATTGTGGAAATTCATCTTGAATCCCATTGTCCTATAGTCCTAG 
3485 178787 ·	Qy 3426 TGTGTTTGAGCAGCATTGACACATATCTGCTTTGATAAGAGACTTCCTGATTCTCTAGGT
3425 178847	Qy 3366 TGTGCCTGTCCCCCAGGTGGTGGGAATAATTTACAATCTGTCCAACCAGAAAGAA
3365 178907	Qy 3306 AACTCATACTAACTGGTTTGGATGCCTGGGTTGTGACTTCTACTGACCGCTAGATAAACG
3305 178967	QY 3246 CTGTGTTATTAAGAGATCAAATGTATAACCACCTAGCTCTTTTCACCTGACTTAGTAAT
3245 179027	Qy 3186 ACTGGGGTCCCCAGGATGAAAACGACAATGTGCCTTTTTATTATTATTATTTAT
3185 179087	QY 3126 CTTGCCCTCTTCAGGACAACAGTTCCAATTCCAAGGAGGCTACCTGAGGTCCCTACTCTC
3125 179147	QY 3066 GGCCTGAGTCACCTAGCATAGGGTTGCAGCAAGCCCTGGATTCAGAGTGTTAAACAGAGG
3065 179207	QY 3006 CAGCTCATGTGCTCCTCAACTTAGGCTGTGCGGTTAGCCAGCC
3005 179267	Qy 2946 GGACTCATTCTAAGGGCAAGACATTGAAAATGATGAATTCCAATCTGGATACAGTCATGA
2945 179327	Qy 2886 ATTATACAGAAGGAACAGCAGGAGGTTTTCCTGGACACCGCCAACTTCACATTGCTCAGT
2885 179387	Qy 2826 ATAAAGCAGGGCACTGAGACACCCGTCCGTGTTTCCTAACCAGAAATCCTAAAGAAGAGA
2825 179447	Qy 2766 TCAGGAGCCCATGGAGCCAGCAGAGAATAACTTGATCCAGTCCAGACGCTTTGCTGAGTTTC
2765 179507	QY 2706 CTCCCATCCCAACAATGGGGATGTAAGCAGCAAGGACACAGACATTCCCTTACTGAACAC
2705 179567	Qy 2646 GGCCACTGAGGAGCCACCTCCTCGCTCCCCTCGCTGAGATCTGAGAGTGAACCGTACACCTT
2645 179627	QY 2586 CATGGGGGTCTGTCCTCCCCCCCCCCCACCATATGCTCCAGGGCCCCAACTGCAAAGTT
179687	

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          CTGTGGTCATTGCACAGAAGGGAAAGGGTCTCAAGGAAGAGTCAACTGGGACAAGCACAAG
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CTGTGGTCATTGCACAGAAGGGAAAGGTCTCAAGGAAGAGTCAACTGGAACAAGCACAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Scie University of Tokyo, Laboratory of Genome Structure Analysis, H Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
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Homo sapiens signet-ring cell carcinoma cell_line:KATO
mRNA, clone_lib:KAT clone:KAT10759.
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Sugano, S., Suzuki, Y., Ota, T., Obayashi,
Shibahara, T., Tanaka, T. and Nakamura, Y.
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NEDO human cDNA sequencing project
Unpublished
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/db_xref="GI:10439515"
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/clone_lib="KAT"
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BASE COUNT ORIGIN Query Match
Best Local Similarity
Matches 3204; Conserv 173 GCGCGCAGGTGAGTGAGCCAGGGGGGGAGCGCAGCTGGGGCCTGGGGCCTTGGGGCCCTGGGGCCCTGGGGCCCCGCGCAGGTGAGCCAGGGCGGAGCGCAGCTGCGCCCGGGCTTGGGCCCTGGGGCCCTGGGGCCCTGGGGCCC 653 421 593 361 533 301 473 181 353 121 721 601 541 481 233 773 61 GTCCTGAGAATCACTTTGTCATAGAGATCCAGAAAAATATTGACTGTATGTCAGGCCCAT ATATAACCATGTTGTCCATCAAGTCTGGAGAAAGAATAGTCTTTACCTTTAGCTGCCAGA GCGGCCGAATCGATGCCACCGTGGTCAGGATCGGAACCTTCTGCAGCAATGGCACTGTGT CTTTCATCTGGGATGTCAAAGCTCATAAGAGCATCGGTTTAGAGCTGCAGTTTTCCATCC GTCCTTTTGGGGAGGTTCAGCTTCAGCCCTCGACATCGTTGTTGCCTACCCTCAACAGAA GTCCTTTTGGGGAGGTTCAGCTTCAGCCCTCGACATCGTTGTTGCCTACCCTCAACAGAA TGAACTGCGGGGTCTCTATCGCACTGCTAGGGGTTCTGCTGCTGCGGGTGCGGCGCCCTGC CCCGGATCAAGATGCAAGAAGGAGTGAAAAATGGCCTTACACCTCCCATGGTTCCACCCCA CCCGGATCAAGATGCAAGAAGGAGTGAAAATGGCCTTACACCTCCCATGGTTCCACCCCA CTCGCCTGAGGCAGATCGGTCCGGGTGAGAGCTGCCCAGACGGAGTCACTCCATCA CTTTCATCTGGGATGTCAAAGCTCATAAGAGCATCGGTTTAGAGCTGCAGTTTTCCATCC TAAAGCTGGGGACCCCGACTCTGCTGGCAAAACCCTGTTACATCGTCATTTCTAAAAGAC TGAACTGCGGGGTCTCTATCGCACTGCTAGGGGTTCTGCTGCTGGGTGCGGCGCGCCTGC GCGGCCGAATCGATGCCACCGTGGTCAGGATCGGAACCTTCTGCAGCAATGGCACTGTGT 789 Conservative /translation="MAGLNCGVSIALLGVLLLGAARLPRGAEAFEIALPRESNITVLI
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PCPFGEVQLQPSTSLLPTLNRTFIWDVKAHKSIGLELQFSIPRLRQIGPGESCPDGVT
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RLCIIESVFEGEGSATLMSANYPEGFPEDELMTWQFVVPAHLRASVSFLNFNLSNCER
KEERVEYYIPGSTTNPEVFKLEDKQPGNNAGNFRISLSCQCDQDAQSPGILRLQFQVUV
QHPQNESKKIYVVDLSNERAMSLTIEBRPVKQSRKFVPGCFVCLESRTCSSNLTILTSG
SKHKISFLCDDLTRLMMNVEKTISCTDHRYCQRKSYSLQVPSDILHLPVELHDFSWKL
LVPKDRLSLVLVPAQKLQQHTHEKFCNTSFSILVASAIPSQDLYEGSFCPGGSIKQIQ
VKQNISVTLRTFAPSFRODAGKTGVSFSILVASAIPSQDLYEGSFCPGGSIKQIQ
VKQNISVTLRTFAPSFRODAGKTTVSFIPYFKEEGYFTVDTDTKSKVYLRTPNWDR
GLPSLTSVSWMISVPRDQVACLTFFKERSGVVCQTGRAEMIIQEQRTRAEEIFSLDED
VLPKPSFHHHSFWVNISNCSPTSGKQLDLLFSVTLTPRTVDLTVILIAAVGGGVLLLS
ALGLIICCVKKKKKTNGGPAVGIYNGFNINTENPRQPKRCKGKRKDNDSHYYAVIEDT
MYGHLLDDSSGSFLQPEVDTYRPFQGTMGVCPPSPPTICSRAPTAKLATEEPPPRSP
PESESEPYTFSHPNNGDVSSKDTDIPLLSTQEPMEPAE"

89 a. 922 c 810 9 703 t 51.9%; 0, Score 3201.6; Pred. No. 0; Mismatches DB 4 9; Indels Length 0 Gaps 720 480 592 472 952 892 660 832 600 540 420 360 532 300 180 352 120 292 60 0

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AK026028
AK026028.1 GI:10438737
AK026028.1 GI:10438737
HOmo sapiens primary human renal epithelial
clone_lib:HRC clone:HRC06785.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shibahara,T., Tanaka,T. and Nakamura,Y.
Direct Submission
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Scie University of Tokyo, Laboratory of Genome Structure Analysis, H Genome Center; Shirokane-dal, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mall:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S. NEDO human cDNA sequencing project
                                                                                                                                                                                                                                                                                                                               NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science,
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Mammalia; Eutheria;
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/db_xref="taxon:9606"
/db_cxef="taxon:9606"
/clone="HROG785"
/cell_type="primary human renal epithelial cells"
/clone_lib="HRC"
/note="cloning vector pME18SFL3"
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3647	8 AGCTGCAGCAATACTTTGACATTTAAAGAGAAATTTAGAGAATATTCTCATCCTCTAAAA	Qy 358	
1140	TGTCCTATAGTCCTAGCAATAAGAGAAATTTCCTCAAGTTTCCATGTGCGGT	Db 108	
3587	TTGTCCTATAGTCCTAGCAATAAGAGAAATTTTCCTCAAGTTTTCCATGTGCGGTTCTCC	Оу 352	
3527 1080	B CTTCCTGATTCTCTAGGTCGGTTCGTGGTATCCCATTGTGGAAATTCATCTTGAATCCC	Oy 346 Db 102	
	CANCCAGAAAAGAATGTGTGTGTTTGAGCAGCATTGACACATATCTGCTTTGATAAGA	9 4	
	CIGACCGCTAGATAAACATGTGCCTGTCCCCCCAGGTGGTGGGAATAATTTACAATCTGT	90 4	
ŏ	TTCACCTGACTTAGTAATAACTCATACTGACTGGTTTGGATGCCTGGGTTGTGACTTC	0 00	
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780	GAGGTCCCTACTCTCACTGGGGTCCCCAGGATGAAAACGACAATGTGCCTTTTTA	Db 72 Ov 322	
3227	TGAGGTCCCTACTCTCACTGGGGTCCCCCAGGATGAAAACGACAATGTGCCTTTTTAT	9	
3167 720	8 CAGAGTGTTAAACAGAGGCTTGCCCTCTTCAGGACAAGTTCCAATTCCAAGGAGCCTA	10	
3107	B CTGTAATGAGGAGAGAGGCCTGAGTCACCTAGCATAGGGTTGCAGCAGCCCTGGATT 	0 4	
3047	ATCTGGATACAGTCATGACACCTCATGTGCTCCTCAACTTAGGCTGTGCGGTTAGCC	298 54	
2987 540	AACTTCACATTGCTCAGTGGACTCATTCTAAG	292	
2927 480	8 AAATCCTAAAGAAGAAGAATTATACAGAAGGAACAGCAGGAGGTTTTCCTGGACACCGCC	N Q	
2867 420	B GACGCTTTGCTGAGTTTCATAAAGCAGGGCACTGAGACACCCGTCCGT	Qу 280 рь 36	
2807 360	B CATTCCCTTACTGAACACTCAGGAGCCCATGGAGCCAGCAGAATAACTTGATCCATTCCA	Qy 274 Db 30	
2747 300	8 GAGTGAACCGTACACCTTCTCCCATCCCAACAATGGGGATGTAAGCAGCAAGGACACAGA	268	
2687 240	8 GGCCCCAACTGCAAAGTTGGCCACTGAGGAGCCACCTCCTCGCTCCCTGCTCCTGAGTCTGA 	Qy 262 Db 18	
2627 180	8 CCGGCCGTTCCAGGCCACCATGGGGGTCTGTCCTCCCTCC	Oy 256 Db 12	
2567 120	8 ATATGGGCATCTGCTACAGGATTCCAGCGGCTCCTTCCTGCAGCCAGAGGTGGACACCTA	Qy 250 Db 6	

REFERENCE AUTHORS	TITLE JOURNAL	REFERENCE AUTHORS	ORGANISM	VERSION KEYWORDS SOURCE	DEFINITION ACCESSION	RESULT 9 AK026187	Db 1861	ОУ 4307	Db 1801	ОУ 4247	Db 1741	Оу 4188	_	Qy 4128	Db 1621	ОУ 4068	Db 1561	ОУ 4008	150	Оу 3948	44	Ov 3888	382	Db 1321	Qy 3768	Db 1261	ОУ 3708	pb 1201	Оу 3648	Db 1141
	Okamoto, S., Okitani, R., Ota, T., Suzuki, Y., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Nakamura, Y., Isogai, T. and Sugano, S. NEDO human cDNA sequencing project Unpublished	; Catarrhini; Hominidae; Homo. take,N., Inagaki,H., Ikema,Y.,	Homo Saplens  Homo Saplens  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;	AK026187.1 GI:10438956 oligo capping; fis (full insert sequence). Homo sapiens primary human renal epithelial cells cDNA to mRNA, clone lib.HRC clone.HRC13020	Homo sapiens cDNA: FLJ22534 fis, clone HRC13020.	מא השפעה ו	AGG	CAGGTCACCACACCCCACACTACGCCCCTATC 4337	TAGCAACAACTGGCTGGAGCTGGGCACCAGCTCTGCCTTTAGAAGGGGTGTCCACTTCAC 1860	AACAACTGGCTGGAGCTGGGCACCAGCTCTGCCTTTAGAAG	ACACTTAAAAAAAAAAACCCAGATCAGAAGATCTGGCCATGCTGGGGCTCACATTCTCACC 1800	ACTT-AAAAAAACCCCAGATCAGAAGATCTGGCCATGCTGGGGCTCACATTC	ACAGGAGAGGCTACAAAATGATCTGGCGCACAGGGATGTTTTGTTTAGCTTGCGGACTCT 1740	AGGAGAGGCTACAAAATGATCTGGC	ACCAGGACATCTTTGGGGTGCTGTTATTCTGCCTACCACACCTTCCTGCCACTGACTCCC 1680	AGGACATCTTTGGGGTGCTGTTATTCTGCCTACCACACCCTTCCTGCCACTGACTC	TCATCATCCTGGAAGAGCCTTTTGCCATGCAAGACAACATAGCCACAGGTGGGGATTAGG 1620	TCATCCTGGAAGAGCCTTTTTGCCATGCAAGACAACATAGCCA		TTTGACTTACAAAGCCCACCAGGAAGATCCAGGATAATCTCTCCATCTAAAGATCC	CAGTGGCTGGTCAAGCTTTTCTCACATGGCATCACTGTGACACTGGCCCTCCCACTTCC 15	AGAGAHARANGANANGANANGANGANGANGANGANGANGANGANGANG	388	AATGGATGTCCCTGAATGAAAATCAAGGTGTCAGCAGAGCTGTGCTCCTTCTGAAGGCTC 1380	AATGGATGTCĆCTGAATGAAAATCAAGGTGTCAGCAGAGCTGTGCTCCTTCTGAAGGCTC 3827	CATTACTTGGTAGCTTAAAAACAACACATTAGCTTATAGTCCTGGGGATCAGAATTCCAA 1320	ATTACTTGGTAGCTTAAAAACACACATTAGCTTATAGTCCTGGGGATCAGAATTC	ATGTTTAAATATATACCAAACAGTGGCCCCCTGCATTAGTTTTCTGTTGCCACTGCAACC 1260	TTTAAATATATACCAAACAGTGGCCCCCTGCATTAGTTTTCTGTTGCCACTGC	

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University of Tokyo, Lak
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MGC:31813 IMAG
BC021099
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                           Submitted (03-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                                                                                             AGGCGTCCCGGAGTCATGGCCGGCCTGAACTGCGGGGTCTCTATCGCACTGCTAGGGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 40 Row: f Column: 14
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 12383093.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Con
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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/protein_id="AAH31099.1"
/protein_id="AAH31099.1"
/db_xref="GI:18088979"
/tamslation="MAGLINCGYSIALLGVLLLGAARLPRGAEAFEIALPRESNITVLI
/translation="MAGLINCGYSIALLGVLLLGAARLPRGAEAFEIALPRESNITVLI
KLGTPTLLAKPCYIVISKRHITMLSIKSGERIVFTFSCQSPENHFVIEIQKNIDCMSG
PCPFGEVQLQPSTSLLDTLNRTFIMDVGAHKSIGLELQFSIPRLYGGIGGESCDBGYT
HSISGRIAMYVRICTFCSNCTYSRIKMQEGVKMALHLPWFHPRNVSGFIANRSSIT
HSISGRIAMYVRICTFCSNCTYSRIKMQEGVKMALHLPWFHPRNVSGFIANRSSIK
RLCIIESVFEGEGSATLMSANYPEGFPEDELMTWQFVVPAHLRASVSFINFNLSNCER
KEERVEYYIPGSTTNPEVFKLEDKQPGNMAGNFNLSLQGCDQDAQSPGILRLQFQVLV
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/db_xref="taxon:9606"
/clone="MGC:31813 IMAGE:4590554"
/tissue_type="Kidney, renal cell
/clone_lib="NIH_MGC_14"
/lab_host="DH10B-R"
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Eutheria;
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Primates;
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TGTGACCAAĠATGCCCAAAGTCCAGGGATCCTCCGGCTGCAGTTCCAAGTTTTGGTCCAA
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Baker,K.P., Beresini,M., Deforge,L., Desnoyers,L., Filvaroff,E., Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L. Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K.,
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t W00140466.
                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
    Gurney, A.L., abe, C.K.,
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/db_xref="taxon:9606"
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AUTHORS
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                                                                    11 Similarity
962; Conser
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Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,
Nakamura,Y., Isogai,T. and Sugano,S.
NEDO human cDNA sequencing project
Unpublished
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Homo Sapiens cDNA: FLJ22676 f
aK026329
                                                                                                                                                                                                                                                                                                                                           NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- 6 3'-end one pass sequencing: Departant of Virology and Human Genome Center, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 976)
Sugano, S., Suzuki, Y., Ota, T., Obayashi, M.,
Shibahara, T., Tanaka, T. and Nakamura, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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                                                                    Conservative
                                                                                                                                                    /tissue_type="human small intestine"
/clone_lib="HSI"
/note="cloning vector pME188FL3"
257 c 219 g 249 t
                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HSI10569"
                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                  15.6%;
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Primates;
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Pred. No. 3.3e-191;
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Query Match
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                            AGCCAGGACCTGTACTTCGGCTCCTTCTGCCCGGGAGGCTCTATCAAGCAGATCCAGGTG 1809
                                                                                                                                           CATACACACGAGAAGCCCTGCAACACCAGCTTCAGCTACCTCGTGGCCAGTGCCATACCC
                                                                                                            CATACGCAAGAGAGGCCTTGTAACACCAGCTTCGGGTACCACGTGACCAGCACCACCCCT
GGCCAGGACCTGTACTTTGGTTCCTTCTGCTCAGGAGGCTCCATCGAGAAGATCCAGGTG
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Direct Submission
Submitted (25-JUL-2001) National Institutes of Health, Mammalian Submitted (25-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Tratitute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://lmage.llnl.gov Series: IRAK Plate: 17 Row: 1 Column: 17 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Baylor College of Medicine Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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Gonaratne, P.H., Garcia, A.M., Lu, X.,
Yoon, V.S., Kowls, C.R., Lawrence, S.,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center code: BCM-HGSC
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VVIGAAGGGALLLFALVLIICFYKKKKKVDKGPAVGIYMGNVPTQMPQTQKFPKGRKD
NDSHVYAVIEDTMVYGHLLQDSGGSFIQPEVDTYRPFQGPMGDCPPTPPPLFSRTPTA
KFTAEELAPSSPPESESSPYTFSHPNKGEIGVRETDIPLHTQGPVETEE"

a 943 c 906 g 979 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="Unknown (protein for IMAGE:3709937)"
/protein_id="AAH11340.1"
/db_xref="GI:15030170"
/translation="ILLYPKDKLSLMLVPGQKLQOHTQERPCNTSFGYHVTSTTPGQDL
YFGSFCSGGSIEKIQVKQNSSYTLRAYAPSFQQEVSKQGLIVSYTPYFKEEGIFTVTP
DTKNKYYLRSPNWDRGLPALSSVSWNISVPSNQVACLTVLKERSGLACQSGRAFMIIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Mammary tumor.ductal carcinoma. 5 month old/clone_lib="NCI_CGAP_Mam6"/lab_host="DH10B"
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1. .3843
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                                                                                                                                                                                                                                                                                                                               Score 821.2; DB 10;
Pred. No. 3e-162;
0; Mismatches 378;
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d virgin mouse."
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Muzny, D.M.,
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                                              AAGCAGGGCACTGAGACACCCGTCCGTGTTCCTAAACCAGAAATCCTAAAGAAGAAGAGGAATT
                                                                                         GGACCAGTGGAGACTGAAGAGTAACTTGGCCCCATTCCAAAGACTTTGCTGAGATGCATG
                                                                                                                                                    CATCCCAACAAGGGGGAGATTGGTGTTAGGGAGACTGACATCCCCTTACTCCATACCCAA
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                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can through the I.M.A.G.E. Consortium/LLML at: http://image.llr Series: IRAK Plate: 44 Row: p Collumn: 21 This clone was selected for full length sequencing because passed the following selection criteria: Hexamer frequency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (02-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BC034137 1999 bp mRNA lin
Mus musculus, similar to hypothetical protein
MGC:33174 IMAGE:5004246, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                              Dickson, M.,
R. M.
                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford,
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://c
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg, R
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Mammalia; Eutheria;
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              /tissue_type="Mammary tumor.
old mouse. Taken by biopsy."
/clone_lib="NCI_CGAP_Mam2"
/lab_host="DH10B"
                                                                                      /map="FVB/N-3"
/clone="MGC:32174 IMAGE:5004246"
 /note-"Vector:
                                                                                                                           /organism="Mus musculus"
/db_xref="taxon:10090"
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Rodentia;
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PCMV-SPORT6"
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Sciurognathi; Muridae;
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SATLMSANYBGGFPEDELMTWQFVYPAHLRASVSFLNFNVSNCERKEERVEYYIPGST
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DLSRERTMSLTIEPRFVKHGRRFVPGCEVCLESRTCSTNVTLTAGSIHKISFLCDDLT
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Xu,J., Lodes,M.J., Secrist,H., Benson,D.R., Stolk,J.A., King,G.E., Wang,T. and Jiang,Y. Compounds for immunotherapy and diagnosis of
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Patent: WO 0149716-A 362 12-JUL-2001;
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US-09-528-706-4
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US-09-528-706-4
US-09-528-706-11
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US-08-276-967-2
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Patent No. 5851817
GENERAL INFORMATION:
                                                                                      Query Match
Best Local S
                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Texas
COUNTRY: USA'
ZIP: 77210-4433
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,967
FILING DATE: Submitted Herewith
CLASSIFICATION: 530
                                                                                                                                                                                                                                            TELEX: 79-0924
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION'NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTSD:418\KIT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713.787-1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, Whi
STREET: P. O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hardy, Daniel M.
APPLICANT: Garbers, David L.
TITLE OF INVENTION: Species-Specific Egg-Binding Proteins
TITLE OF INVENTION: Sperm
                                                                                                                                                                                                                                                                         TELEFAX: /15
TELEFAX: 79-0924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                   484 VASAIPSQDLYFGSFCPGGSIKQIQVKQN------
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                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                        TELEPHONE: 713-70,
85 VLGSIRKHTLESGQ--PGPSWQPVSVNYTSQGQIQFTLVGVFGKIPEPAVAVDAISIAPC 142
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                                                                                                                                                                                                                               2476 amino acids
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Garbers, David L.
                                                                        Conservative
                                                                                                                                                            protein
                                                                                                                                                                                              single
                                                                                      2.7%; Score 117;
21.6%; Pred. No. 0.
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US-09-286-891-2
US-08-899-008-5
US-08-453-472-8
US-08-038-948-5
US-08-038-948-5
US-08-08-39-952-8
US-08-862-903-8
US-08-862-903-8
US-08-862-903-8
US-08-862-903-9
US-08-859-568-2
US-08-859-568-2
US-09-528-706-2
US-09-528-737-93
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US-08-450-751-2
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                                   ----ISVTLRTFAP- 522
                                                                        Indels 148;
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Scoring table:

Title: Perfect score:

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                                 INFORMATION FOR SEQ ID NO:
                                                                 FILING DATE: 28-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kenneth D Sibley
REGISTRATION NUMBER: 31,665
                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/755,58
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SEQUENCE CHARACTERISTICS:
LENGTH: 1589 amino aci
                                                                                                                                     FILING DATE: 14-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                FILING DATE: 25-NOV-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ashworth, Alan APPLICANT: Stratton, Michael R
                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               523
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CITY: F
                           REGISTRATION NUMBER: 540
REFERENCE/DOCKET NUMBER: 540
REFERENCE/DOCKET NUMBER: 540
                                                                                                                                                                                                                                APPLICATION NUMBER: GB 9 FILING DATE: 23-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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310 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Futreal, Phillip
Wooster, Richard
                                                                                                                                                                                                                                                                                      25-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Materials and methods relating to the identification and sequencing of the susceptibility gene and uses thereof.
                                                                                                                                           GB 9617961.9
                                                                                                                                                                                               GB 9525555.0
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US-08-459-568-4

Sequence 4, Application Patent No. 5811304 GENERAL INFORMATION:

US/08459568

APPLICANT: Huang, Shi TITLE OF INVENTION: Retino TITLE OF INVENTION: Zinc F NUMBER OF SEQUENCES: 93 CORRESPONDENCE ADDRESS:

Retinoblastoma Protein

Interacting

Finger

Proteins

ADDRESSEE: STREET: 4

1: Campbell at 4370 La Jolla

l and Flores lla Village [

Drive,

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; TOPOLOGY: linear
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Best Local Similarity
                                                 1124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198 LPWFHPRNVSGF-----SIANRSSIKRLCIIESVFEGEGSATLMSANYPEGFPEDEL
                                                 SPRVSATKERNLHPQTINYCVQKLETNTSPHANKDVAI 1161
                                                                                                                                                                                                                                                                                       LIAAVGGGVLLLSALGLIICCVKKKKKKTNKGPAVGIYNGNINTEMPRQPKKFQKGRK--
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                                                                                 EPPPRSPPESESEPYTFSH-----PNNGDVSSKDTDI
                                                                                                                  CHSYLSQSSFCHCDDMHNDSGYFLKNKIDS------DVPPDM----KNAEGNTI
                                                                                                                                                    VYGHLLQDS------SGSFLQPEVDTYRPFQGTMGVCPPSPPTICSRAPTAKLATE
                                                                                                                                                                                                                                                                                                                          KCEEMQNFVSKETEMLPQQNYHMYRQTENLKTSNGTSSKVQENIENNVEKNPR-----
                                                                                                                                                                                                                                                                                                                                                                                                                          SKYYLR-TPNWDRGLPSLTSVSWNISVPRDQVACLTFFKERSGVVCQTGRAFMIIQEQRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IKQIQVKQNISVTLRTFAPSFQQEASRQGLTVSF-----IPYFKE--EGVETVTPDTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TDELTVISDSLNSKILHGINKDKMHTSCHKK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --KLLVPKDRL-SLVLVPAQKLQQHT--HEKPCNTSFSYLVASAIPSQDLYFGSFCPGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T------CMKSSDKKQLPSDKMEQNIKEFNISFQTASGKNTRVSKESLNKSVNIFNRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMSLITIEPRPVKQSRKFVPGCFVCLESRTCSSNLTLTSGSKHKISFLCDDLTRLWMNVEK 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDKQPGNMAGNFNLSLQGCDQDAQSPGILRLQFQVLVQHPQNESNKIYV----VDLSNER
                                                                                                                                                                                    REQGDKLGTRNTIKIECKEHTEDFAGNASYEHSLVIIRTEIDTNHVSENQVSTLLSDPNV
                                                                                                                                                                                                                      ----DNDSHVYAVI----
                                                                                                                                                                                                                                                       ------SLSKGRKWL
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17.7%; Pred. No. 0.11;
tive 105; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233;
                                                                                 823
                                                                                                                                                                                                                  -----EDTM 741
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; LENGTH: 1719 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-459-568-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Versi.
APPLICATION UMBER: US/08/459,568
FILING DATE: 02-JUN-1995
CLASSIFICATION UMBER: US 08/399,411
PRIOR APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1264
TELEPHONE: (619) 535-99001
TELEFAX: (619) 535-9949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1719 amino acids
TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177 FC-----SNGTVSRIKMQEG-------VKMALHLPWFHPRNVSGF 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 SIGLELQFSIPRLRQ------IGPGESCPDGVT--HSISGRIDATVVRIGT 176
545 GVFTVTPDTKSKVYLRTPNWDRGLPSLTSVSWNIS--VPRDQVACLTFFKERSGVVCQTG 602
                                                                      740 SPPSSPQH-----
                                                                                                                                                           691 LKQLLQTQDKLTPPAGISATEIAKLGP----VCVSAPASML------PVTSSRFKRRTS
                                                                                                                                                                                                                                             647 LPKIKAETDSDPMVPSCSLSLPLSISTTEAVSF------HKEKSV-----YLSSK
                                                                                                                                                                                                                                                                         375 FYCLESRT-----CSSNLTLTSGSKHKISFLCDDLTRLWMNVEKTISCTDHRYCQRK 426
                                                                                                                                                                                                                                                                                                                               590 SASADLYGINCLLTPVTVEITQNIKTTQVPVTEDLPKEPLGSTNSE---AKKRRTASPPA 646
                                                                                                                                                                                                                                                                                                                                                           317 DQDAQSPGILRLQFQVLVQHPQN-ESNKIYVV-DLSNERAMSLTIEPRPVKQSRKFVPGC 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 SVSFLNFNLSNCERKEERVEYYIPG-----STTNPEVFKLEDKQPGNMAGNFNLSLQGC 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               514 GYRRKGGLE-----EPQPPAEQAQATQNVYVPSTEPEEEGEADDVYIMD-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210 SIANRSSIKRLCIIESVFEGEGSATLMSANYPEGFPEDE-----LMTWQFVVPAHLRA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  454 DCLIMNSEKASODTINSSVVEENGEVKELHPCKYCKKVFGTHTNMRRHQRRVHERHLIPK 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        394 YCGKAFGTQINRRRHERRHEAGLKRKPSQTLQPSEDLADGKASGENVASKDDSSPPSLGP 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               358 FMFPCQHCERKFTTKQGLERHMHIH------ISTVNHAF-----KCK 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 FTFSCQSPENHFV----IEIQKNIDCMSGPCPFGEVQLQPSTSLLPTLNRTFIWDVKAHK 133
                                                                                                           AIPSQDLYFGSFCPGGSIKQIQVKQNISVTLRTFA-PSFQQEA-SRQGLTVSFIPYFKEE 544
                                                                                                                                                                                                  SYSLOVPSDILHLPVELHDFSWKLLVPKDRLSLVLVPAQKLQQHTHEKPCNTSFSYLVAS 486
                                                                                                                                                                                                                                                                                                                                                                                                                           ----ISSNIS-----ENLNYYIDGKIQTNNNTSNCDVIEME------
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California
                                                                    ·SPALRDFGKPSDGKAAWTDAGLT------
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	HSISGRIDATVVRIGT 176	IGLELQFSIPRLRQIGPGESCPDGVTH	134 SIGI 	Qy
	ISTVNHAFKCK 393	OHCERKETTKOGLERHMHIH	358 FMFF	DЬ
	PTLNRTFIWDVKAHK 133	FTFSCQSPENHFVIEIQKNIDCMSGPCPFGEVQLQPSTSLLPTLNRTFIWDVKAHK	78 FTFS	Qy
42;	Length 1719; Indels 333; Gaps	Match 2.5%; Score 110.5; DB 2; Local Similarity 19.1%; Pred. No. 0.46; es 169; Conservative 96; Mismatches 289;	Query Match Best Local s Matches 169	M B Q u
		TOPOLOGY: linear LECULE TYPE: protein 99-411-4	TOPOLOGY MOLECULE 7 08-399-411-4	
		amino acid	TYPE:	٠. ٠.
		HARACTERISTI	SEQUENCE CE	
		(619) 535-8949	TELEFAX:	
		H	TELECOMMUNICATION	
		BER: 31,815	REGISTA	
		FORMATION:	ATTORNEY,	
		APPLICATION NUMBER: US/08/399,411 FILING DATE: 06-MAR-1995 CINCENTIAL 620	APPLICA FILING	
		LICATION DATA:	CURRENT F	٠. ٠
		SYSTEM: PC-DOS/MS-DOS  PatentIn Release #1.0. Version #1	OPERATING	
		PH	MEDIUM TY	
		2122 READABLE FORM:	ZIP: 9	·· ··
		California Y: USA	STATE: COUNTRY:	٠. ٠.
		erra Attraga Citae, Saira	CITY: :	•• •
		ll and Flores	ADDRESSEE:	
		SEQUENCES: 93	NUMBER OF	
	teracting	TITLE OF INVENTION: Retinoblastoma Proteins Title OF INVENTION: Zinc Finger Proteins	TITLE OF	
	•	shi	APPLICANT	0
				Pa
		Application US/08399411	3-08-399-411- Sequence 4,	US-0
				9561
	VE 1039	PLPAPSSSASHPCPSPLSNATAQSPLPILSPTVSPSPSPIPPVE	995 PLP#	Db
	AE 836	- Ħ	795 PRSP	Qy
	SPPPCPPVLTVATPPPPLLPTV 994	TPDVCPSSPALQTPSLSSGQLPPLLIPTDPSSPPPCPP	941 S	Db
	APTAKLATEEPP 794	ICSR	761 TYRE	Qy
	-LGPGSG-FPAPTVE 940	NGIDLPVENPADGTRSPSPCKSLEAQPDPD	898 NGID	Ъ
	HVYAVIEDTMVYGHLLQDSSGSFLQPEVD 760	NINTEMPRQPKKFQKGRKDNDSHVYAVIEDTMVYGH	708 NG-N	Qy
	CSAVKKRKPTTCMLQKVLLNEY 897	FKESHSVQPT	866 FKES	Ф
	KKTNKGPAVGIY 707	LDLLESVTLTPRTVDLTVILIAAVGGGVLLLSALGLIICCVKKKKKKN-	651 LDLI	QУ
	DLSVHKKHCSDSEGKE 865	AFSSVCNQQPLDLSSGVKQKAEGTGKTPVQWESVLD	814 SAFS	Db
	EDVLPKPSFHHHSFWVNISNCSPTSGKQ 650	RAFMIIQEQRTRAEEIFSLDEDVLPKPSFHHHS	603 RAF	γQ
	PCFDEYKMSKEWTAS 813	SKKSKLESHSDSPAWSLSGRDERETVSPPCFDEYKMSKEWTAS	771	В

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RESULT 5
US-08-516-859A-4
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                                                                                                                                                                Sequence 4, Application US/08516859A
Patent No. 6069231
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein -
TITLE OF INVENTION: Zinc Finger Proteins
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                          995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          691 LKQLLQTQDKLTPPAGISATEIAKLGP----VCVSAPASML-----PVTSSRFKRRTS
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                                    COUNTRY:
ZIP: 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         708
                                                                                                      STREET:
                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                        PLPAPSSSASPHPCPSPLSN--ATAQSPLPILSPTVSPSPSPIPPVE 1039
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYRPFQGTMGVCPPSP----PTICSR-------APTAKLATEEPP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPKIKAETDSDPMVPSCSLSLPLSISTTEAVSF------HKEKSV-----YLSSK
                                                                                                                                                                                                                                                                                                                                                                       PRSPPESESEPYTFSHPNNGDVSSKDTDIPLLN----TQEPMEPAE 836
                                                                                                                                                                                                                                                                                                                                                                                                       S----TPDVCPSSPALQTPSLSSGQLPPLLTPTDPSSPPPCPPVLTVATPPPPLLPTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGIDLPVENPADGTRSPSPCKSLEAQPDPD-------LGPGSG-FPAPTVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NG-NINTEMPR-----QPKKFQKGRKDNDSHVYAVIEDTMVYGHLLQDSSGSFLQPEVD 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FKESHSVQPT-----CSAVKKRKPTTCMLQKVLLNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAFSSVCNQQPLDLSSGVKQKAEGTGKTPVQWESVL-----DLSVHKKHCSDSEGKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RAFMIIQEQ------RTRAEEIFSLD---EDVLPKPSFHHHSFWVNISNCSPTSGKQ 650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FVCLESRT-----CSSNLTLTSGSKHKISFLCDDLTRLWMNVEKTISCTDHRYCQRK 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SASADLYGINCLLTPVTVEITQNIKTTQVPVTEDLPKEPLGSTNSE---AKKRRTASPPA 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DQDAQSPGILRLQFQVLVQHPQN-ESNKIYVV-DLSNERAMSLTIEPRPVKQSRKFVPGC
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                                    92122
                                                                   San Diego
: California
                                                                                                    E: Campbell & Flores LLP 4370 La Jolla Village Drive, Suite 700
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Best Local Similarity 19.1%; Pred. No. 0.46;
Matches 169; Conservative 96; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (619) 535-89 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/292,683 FILING DATE: 18-AUG-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US OF FILING DATE: 06-MAR-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  358 FMFPCQHCERKFTTKQGLERHMHIH--------ISTVNHAF------KCK 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 FTFSCQSPENHFV----IEIQKNIDCMSGPCPFGEVQLQPSTSLLPTLNRTFIWDVKAHK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/516,859A FILING DATE: 18-AUG-1995
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                  RAFMIIQEQ------RTRAEEIFSLD---EDVLPKPSFHHHSFWVNISNCSPTSGKQ
                                      -----SKKSKLESHS------DSPAWSLSGRDERETVSPPCFDEYKMSKEWTAS
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                                                                       GVFTVTPDTKSKYYLRTPNWDRGLPSLTSVSWNIS--VPRDQVACLTFFKERSGVVCQTG
                                                                                                                                                                                                                            SYSLQVPSDILHLPVELHDFSWKLLVPKDRLSLVLVPAQKLQQHTHEKPCNTSFSYLVAS
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amino acid
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                                                                              US-09-586-472-4
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Patent No. 6323335
PATENT INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: RA
Query Match
Best Local Similarity
Matches 169; Conserv
                                                                                                                                                                         TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1719 amino acids
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                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 4130
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   995 PLPAPSSSASPHPCPSPLSN--ATAQSPLPILSPTVSPSPSPIPPVE 1039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/586,472
FILING DATE: 01-Jun-2000
CLASSIFICATION: CUNKNOWN>
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NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Diego
STATE: California
                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 09/528,706
FILING DATE: 17-MAR-2000
APPLICATION NUMBER: US 08/516,859
FILING DATE: 18-AUG-1995
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COUNTRY: USA
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  Conservative
                  2.5%;
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Zinc Finger Proteins
96; Mismatches
                Score 110.5; D
Pred. No. 0.46;
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                                      Length 1719;
Indels 333;
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Gaps
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42;
              Sequence 4, Application US/09528706
Patent No. 6468985;
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastom
TITLE OF INVENTION: Zinc Finger P
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                       RESULT 7
US-09-528-706-4
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ADDRESSEE:
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                                                                                                                                                                                                                                                    PLPAPSSSASPHPCPSPLSN--ATAQSPLPILSPTVSPSPSPIPPVE 1039
                                                                                                                                                                                                                                                                                         PRSPPESESEPYTFSHPNNGDVSSKDTDIPLLN----TQEPMEPAE 836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----SKKSKLESHS------DSPAWSLSGRDERETVSPPCFDEYKMSKEWTAS
                                                                                                                                                                                                                                                                                                                                 TPDVCPSSPALQTPSLSSGQLPPLLIPTDPSSPPPCPPVLTVATPPPPLLPTV 994
Campbell & Flores LLF
                                  Retinoblastoma Protein Zinc Finger Proteins: 106
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PRIOR APPLICATION UNBER: US 08/292,6
FILING DATE: 18-80G-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
NAME: Campbell, Data 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.5%; Score 110.5; D
Best Local Similarity 19.1%; Pred. No. 0.46;
Matches 169; Conservative 96; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: P-I-TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER:
487 AIPSQDLYFGSFCPGGSIKQIQVKQNISVTLRTFA-PSFQQEA-SRQGLTVSFIPYFKEE 544 : | | | ; | ; | ; | | |
                                                              691 LKQLLQTQDKLTPPAGISATEIAKLGP----VCVSAPASML------PVTSSRFKRRTS
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TYPE: amino acid
TOPOLOGY: linear
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                                                                                                    SYSLOVPSDILHLPVELHDFSWKLLVPKDRLSLVLVPAQKLQQHTHEKPCNTSFSYLVAS
                                                                                                                                                                           FVCLESRT-----CSSNLTLTSGSKHKISFLCDDLTRLWMNVEKTISCTDHRYCQRK 426
                                                                                                                                                                                                                                 SASADLYGINCLLTPVTVEITQNIKTTQVPVTEDLPKEPLGSTNSE---AKKRRTASPPA 646
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	262	217 IKRLCIIESVFEGEGSATLMSANYPEGFPEDELMTWQFVVPAHLRA	Qy
	1135	TLSKNVEMAHQKKEDPVPLRAENPDLSSSKIPFLPD	Db .
	216	169 ATVVRIGTECSNGTVSRIKMQEGVKMALHLPWFHPRNVSGFSIANRSS	οy
	1082	116 LPTLNKTETHUVKAHKSIGLELGESLEKLIGIGGESCEDGVEHSISGKID	gg dg
38;	sd	atch 2.4%; Score 106.5; DB 4; Leng cal Similarity 18.2%; Pred. No. 2; 150; Conservative 108; Mismatches 283; Inde	M. B.O.
		DENOTH: 2943 TYPE: PRT ORGANISM: Canis familiaris 19-324-867-2	70
		RE: PatentIn V NO 2	S
		EARLIER FILING DATE: 1997-03-06 NUMBER OF SEQ ID NOS: 63	
		EARLIER FILLING DATE: 1998-03-059 EARLIER APPLICATION NUMBER: 60/039,953	
		APPLICATION NUMBER: US/09/324 FILING DATE: 1999-06-03	
	Use	IITLE OF INVENTION: Canine Factor VIII Gene, Protein and Methods of IIIE REFERENCE: 1669.0010002/JAG/BJD	
		L. Suz	
		APPLICANT: Cameron, Cherie APPLICANT: No. 62516321ey, Colleen	
		NERAL INFORMATION: NPPLICANT: Lillicrap, David	
		SULT 8 1-09-324-867-2 Sequence 2, Application US/09324867A Patent No. 6251332	लं ल
		995 PLPAPSSSASPHPCPSPLSNATAQSPLPILSPTVSPSPSPIPPVE 1039	Db
		795 PRSPPESESEPYTFSHPNNGDVSSKDTDIPLLNTQEPMEPAE 836	Qy
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	794	CSRAPTAK	Qy
	940	898 NGIDLPVENPADGTRSPSPCKSLEAQPDPDLGPGSG-FPAPTVE	DЬ
	760		Qy
	897	866 FKESHSVQPTCSAVKKRKPTTCMLQKVLLNEY	DЬ
	707	651 LDILLESYTLTPRTVDLTVILIAAVGGGVLLLSALGLIICCVKKKKKKKTNKGPAVGIY	Qy
	865	814 SAFSSVCNQQPLDLSSGVKQKAEGTGKTPVQWESVLDLSVHKKHCSDSEGKE	Дb
	650	KPSFHHHSFWVNISNCSPTSGK	ρ
	813	771SKKSKLESHSDSPAWSLSGRDERETVSPPCFDEYKMSKEWTAS	Дb
	602	545 GVFTVTPDTKSKVYLRTPNWDRGLPSLTSVSWNISVPRDQVACLTFFKERSGVVCQTG	Qy
	770	740 SPPSSPQHSPALRDFGKPSDGKAAWTDAGLT	ф

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US-08-473-750-1
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APPLICANT: Green, Bruce A.
APPLICANT: Brinton, Jr., Charles C.
APPLICANT: Brinton, Sequence and Analysis of LKP Pilin Patent No. 5834187
Patent No. 5834187 5786143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application Uppatent No. 5834187
Patent No. 5834187 5786143
                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Structural Gene and the LKP TITLE OF INVENTION: Haemophilus Influenzae NUMBER OF SEQUENCES: 21
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                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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  PRIOR APPLICATION DATA: APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                     CITY: Lexington
                                                              APPLICATION NUMBER: US/08/473,750 FILING DATE: 07-JUN-1995
                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                 STATE: Massachusetts
                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EWKSQKKSQTNTAFKR---KDTILPLGPCENNDSTAAINEGQD--KPQREAMWAKQGEPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLLSALGLIICCVKKKKKTN-------KGPA--VGI--YNGNINTEMPRQ
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                                                                                                                                                                                                                                           02173
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                                                                                                                                                                                                                                                                                                                            Two Militia Drive
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    US 08/277,321
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US-08-477-326-11
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Best Local Similarity 20.7
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Green, Bruce A.
APPLICANT: Brinton, Jr., Charles C.
APPLICANT: Brinton, Jr., Charles C.
TITLE OF INVENTION: Sequence and Analysis of LKP Pilin
Patent No. 5968769
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/08477326 Patent No. 5968769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                             ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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REFERENCE/DOCKET NUMBER: ACC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
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ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice O.
                                                                                                                                                                                                              NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281 VEYYIPGSTTNPEVFKLEDKQPGNMAGNFNLSLQGCDQDAQSPGILRLQFQVLVQHPQNE 340
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                                                                                                                         CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 AKPCYIVISKR-HITMLSIKSGERIVFTFSCQSPENHFV----IEIQ---KNIDCMSGP 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                       COUNTRY:
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Haemophilus Influenzae
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                                                                                                                                                                                            Smith & Reynolds,
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US-09-213-293D-1
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                                                                                                                                                                                                           Sequence 1, Application US/09213293D Patent No. 6384299 GENERAL INFORMATION:
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APPLICANT: LOPEZ, PAULA S.
TITLE OF INVENTION: PLANT RETINOBLASTOMA-ASSOCIATED
FILE REFERENCE: 604-469
CURRENT APPLICATION NUMBER: US/09/213,293D
CURRENT FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: PCT/ES96/00130
PRIOR FILING DATE: 1996-06-13
PRIOR APPLICATION NUMBER: PCT/EP97/03070
                                                                                                                                 APPLICANT:
APPLICANT:
                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                     APPLICANT: GUTIERREZ-ARMENTA, CRISANTC
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TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: AC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEPAX: 617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: July 19, 19, ATTORNEY/AGENT INFORMATION: NAME: Carroll, Alice O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 07-JUI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VEYYIPGSTTNPEVFKLEDKQPGNMAGNFNLSLOGCDQDAQSPGILRLQFQVLVQHPQNE
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                                                                                                                                                                                                                                                                                                                                                                                                                  -NTPKIILKKQQRRCTLNNAPVSPNPVK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNKIYVVDLSNERAMSLT---IEPRPVKQSRKFVPGCFVCLESRTCSSNLTLTSGSKHKI
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                                                                                                                                                      XIE, QI
                                                                                                                                                                    SANZ-BURGOS, ANDRES
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NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN VEr. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 683
TYPE: PRT
ORGANISM: Unknown (FEATURE:
649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        270 NLSNCERKEERVEYYIPGSTTNPEVFK-----LEDKQPGNMAGNFNLSLQGCDQDAQSPG 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 VQMTPVTSAMTTAKWLREVISSLPDKPSSKLQ-QFL-----SSCDRDLTNAVTER 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 2.4%;
Local Similarity 19.3%;
les 146; Conservative 9
                                                                                                         LLSALGLIICCVKKKKKKTNKGPA--VGIYNGNINTEMPRQPKKFQKGRKDNDSHVYAVI 737
                                                                                                                                                                 SIDEDVLPKPSEHHHSEWVNISNCSPTSGKQLDLLFSVTLTPRTVDLTVILIAAVGGGVL 679
                                                                                                                                                                                                                                                            WNISVPRDQVACLTFFKERSGVVCQTGRAFMII-----QEQRTRAEEI-----F
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                                                                                                                                                                                                                                                                                                                                                                        IRNLCERVQCVEQTERVYNVFKQILEQQTTLFFNRHIDQLILCCLYGVAKVCQ----LEL 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDNADPRSPKRSCNESRNTVVERNLQTPPPKQSHMVSTS-----LKAKCHPLQSTFASPT 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILRLQFQVLVQHPQ--NESNKIYVV------DLSNERAMSLTIEPRPVKQSRKFVPG- 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLSKI-----IENFVRHEETLPRELKRHLNSLEEQLLESMAWEKGSSLYN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRAELQNSNVNNLTPLLSN--ERFHRCLIACSADLVLATHKTVIMMFPAVLE-STGLTAF 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CIIESVFEGEGSATLMSANYPEGF-----PEDELMTWQFVV---PAHLRASVSFLNF 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V--SIVLEAIFPTKSSANR-----GVSLGLNCANAFDIPWAEARKVEASKLYYR-VLEAI 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDATVVRIGTECSNGTVSRIKMQEGVKMALH-----LPWFHPRNVSGFSIANRSSIKRL 220
SDSVVAGSLGQINGGSTSDPAAAFSPLSKKRETDT
                                  EDTMVYGHLLQDSSGSFLQP-----EVDT 761
                                                                                                                                                PNLPDMSPKKVSASHNVYV-----SPLRQTKLDLLLSPS-----SRSFYACIGEGT-
                                                                                                                                                                                                                       -----RHVGIITFYNE---VFVPAAKPFLVSLISSGTHPEDKKNASGQIPGSPKPSPF
                                                                                                                                                                                                                                                                                                                                                                                                           LQQHTHEKPC--NTSFSYLVASAIPSQD--LYFGSF-----CPGGSIKQIQVKQNISV 515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----VEKTISCTDHRYCORKSYSLOVPSDILHLPVELHDFSWKLLVPKDRLSLVLVPAOK 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----CFVCLESRTC-----SSNLTLTSGSKHKISFLCDDLTRLWMN-- 410
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                                                                         ----HAYQSPSKDLAAINSRLN-----YNGRKVNSRLNFDMV
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Pred. No. 0.29;
8; Mismatches
                                                                                                                                                                                                                                                                                                 -----CKPEVFSSIYIGSTNRNGVLVS----
683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plant RB protein
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RESULT 12 US-08-839-008-2 ; Sequence 2, Application US/08839008 ; Patent No. 5916758

GENERAL INFORMATION

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,008
FILLING DATE: 23-APR-1997
CLASSIFICATION UDBER: 08/563,697
FILING DATE: 28-NOV-195
FILING DATE: 28-NOV-195
INTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50384
TELECOMMUNICATION INFORMATION:
TELECHONE: 610-270-5096
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local (
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TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 449 anino acids
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CORRESPONDENCE ADDRESS: ADDRESSEE: Smithkline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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APPLICANT: Yue, Tian-Li
TITLE OF INVENTION: Smooth Muscle Cell-Derived Migration Factor
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                                                                                                                                                                                                                   165 KAQGTLTTPNWPESDYPPGISCSWHIIAPPDQVIALTFEKEDLEPDTYC--RYDSVSVFN 222
                                                                                                                                                                                                                                                                                                                           179 -----SNGTVSRIKMQEGVKMALHLPWFHPRNVSGFSIANRSSIKRLCIIESVFEG---- 229
                                                                                                                                                                                                                                                                                                                                                                                                      151 PGESC-----PDGVTHSISGRI------DATVV------RIGTFC-----
325 --- TGTLQSNFCASSLVVTATVKSMV 347
                                                                     273 LPRGTAKEGOGPGPKRGTEPKVKLPPKSOPPE-----KTEESPSAPDAPTCPKQCRR--
                                                                                                314 --QGCDQDAQSPGILRLQFQVLVQHPQNESNKIYVVDLSNERAMSLTIEPRPVKQSRKFV 371
                                                                                                                                                                                                                                                                                            119 PLVAPGNQVTLRMTTDEGTGGRGFLLWYSGRATSG------TEHQFCGGRLE 164
                                                                                                                                              223 GAVSDDSRRLGKFCGDAVPGSISS------EGNELLVQFVSDLSVTADGFSASYKT 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 709 Swedeland CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                     59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U
                                  PGCFVCLESRTCSSNLTLTSGSKHKI 397
                                                                                                                                                                                                                                                      EGSATLMSANYPEG-FPEDELMTWQFVVPAHLRASVSFLNFNL---SNCERKEERVEYY- 284
                                                                                                                                                                                                                                                                                                                                                                   PNKECIWTITVPEGQTVSLSFRVFDLELHPACRYDALEVFAGSGTSGQRLGRFCGTFRPA 118
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Rosen, Craig A
Siemens, Ivo R
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                                                                                                                                                                                -----IPGSTTNPEVFKLEDKQPGN-------MAGNFNLSL-- 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            41; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 104; DB Pred. No. 0.19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 449;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Оу	Дb	νg	Db	Qy	Db	Qy	Db .	0 <b>v</b>	Db dd	Qγ	Qu Be	vs-						 								•••					٠. ،			٠.		٠.		٠,٠	,	RES US-
400 LCDDLTRLWMNVEKTISCTDHRYCQRKSYSLQVPSDILHLPVELHDESWKLLVPKDR 456	239 EVNAEKVVGNMKPPKPTKIKKKGVKKTFQCELCSYTCPRRSNLDRHMKSHTDERPHK-CH 297	348 DLSNERAMSLTIEPRPVKQSRKFVPGCFVC-LESRTCSSNLTLTSGSKHKISF 399	219 KDVDVSVYDFEEE 238	288 STINPEVFKLEDKQPGNMAGNFNLSLQGCDQDAQSPGILRLQFQVLVQHPQNESNKIYVV 347	171 ANGEVETLEQGELPPQEDPSWQKDPDYQPPAKKTKKTKKSKLRYTEEG 218	245PEDELMTWQFVVPAHLRASVSFLNFNLSNCERKEERVEYYIPG 287	QLVQVPVPVTVPVATTSVEELQGAYENEVSKEGLAESEPMICHTLPLPEGFQVVKVG	ур	aeaavddtqiitlqv	166 RIDATVVRIGTECSNGTVSRIKMQEGVKMALHLPWFHPRNVSG	Query Match 2.4%; Score 103.5; DB 2; Length 727; Best Local Similarity 16.4%; Pred. No. 0.51; Matches 133; Conservative 99; Mismatches 261; Indels 319; Gaps	MOLECULE TYPE 08-475-844-9	TYPE: amino acid TOPOLOGY: linear	H: 727	INFORMATION FOR SEQ ID NO: 9:	TELEPHONE: 206-467-9600 TELEPAX: 415-543-5043	REFERENCE/DOCKET NUMBER: 14538A-11-1 TELECOMMUNICATION INFORMATION:	NAME: Darmaloo Storen W	0	APPLICATION NUMBER: 08/261,680	CLASSIFICATION: 536 PRIOR APPLICATION DATA:	7.	CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/475,844	ease	OPERATING SYSTEM: PC-DOS/MS-DOS	TYPE: Flo	COMPUTER READABLE FORM:	Ħ	STATE: CA	STREET: One Market Plaza	Ď	CORRESPONDENCE ADDRESS: 21	0 1/	Filippova, Galin	APPLICANT: KLEHOVA, ELEHA M. APPLICANT: Goodwin, Graham H.	Neiman, P	APPLICANT: Lobanenkov, Victor V.	Į.	Sequence 9, Application US/08475844	S-08-475-844-9

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RESULT 14
PCT-US95-08429-9
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GENERAL INFORMATION:
APPLICANT:
           Query Match
                                                                                                            TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: CTC)
NUMBER OF SEQUENCES: 21
COMPUTER READABLE FORM:
MEDIION TYPE: Floppy di
COMPUTER: IBM PC compa
                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 17-JUN-1994
                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                  MOLECULE TYPE:
                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 206-467-9600
                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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 Local
                                                           TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                            NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14538A-11-1PC
                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 15-JUI CLASSIFICATION:
                                                                                   LENGTH:
                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
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 Similarity
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                                                                                 727 amino acids
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SYSTEM: PC-DOS/MS-DOS
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2.4%;
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 Score
Pred.
 103.5;
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RESULT 15
US-08-839-008-9
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                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF I
                                                                APPLICANT:
                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 RIDATVVRIGTFCSNGTVSR------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KVYLRTPNWDRGLPSLTSVSWNISVPRDQVA-----CLTFFKERSGVVCQTGRAFMII 608
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SEQUENCES:
                       Siemens, Ivo R
Siemens, Ivo R
Young, Peter R
Yue, Tian-Li
VENTION
                                                                                                       McDonnell, Peter
McNulty, Dean E
Rosen, Craig A
                                                                                                                                                                          Hurle, Mark
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  Smooth Muscle Cell-Derived Migration Factor \boldsymbol{9}
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Search completed: November 11, 2002, 11:34:18 Job time : 31 secs
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ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,008
FILING DATE: 23-APR-1997
CLASSIFICATION: 435
CLASSIFICATION: 435
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APPLICATION NUMBER: 08/563,697
FILING DATE: 28-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50384
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                     179 -----SNGTVSRIKMQEGVKMALHLPWFHPRNVSGFSIANRSSIKRLCIIESVFEG---- 229
                                                                               325 --- TGTLQSNFCASSLVVTATVKSMV 347
                                                                                                    372 PGCFVCLESRTCSSNLTLTSGSKHKI 397
                                                                                                                                                    273 LPRGTAKEGOGPGPKRGTEPKVKLPPKSOPPE-----KTEESPSAPDAPTCPKOCRR--
                                                                                                                                                                                                314 -- QGCDQDAQSPGILRLQFQVLVQHPQNESNKIYVVDLSNERAMSLTIEPRPVKQSRKFV 371
                                                                                                                                                                                                                                                                                                                   165 KAQGTLTTPNWPESDYPPGISCSWHIIAPPDQVIALTFEKFDLEPDTYC--RYDSVSVFN 222
                                                                                                                                                                                                                                                                                                                                                                                                   119 PLVAPGNOVTLRWTTDEGTGGRGFLLWYSGRATSG-----SEHQFCGGRLE 164
                                                                                                                                                                                                                                        223 GAVSDDSRRLGKFCGDAVPGSISS------EGNELLVQFVSDLSVTADGFSASYKT 272
                                                                                                                                                                                                                                                                                230 EGSATLMSANYPEG-FPEDELMTWQFVVPAHLRASVSFLNFNL---SNCERKEERVEYY- 284
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CITY: King of Prussia
STATE: PA
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Title: Perfect score: Sequence:

Run on: OM protein -

Scoring table:

Minimum DB Maximum DB

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match
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APPLICANT: No. US20020142003Albert Schweifer
APPLICANT: Marwa Scherl-Mostageer
APPLICANT: Molfgang Sommergruber
APPLICANT: Roger Abseher
ITITLE OF INVENTION: Tumorassoziiertes Antigen (B345)
FILE REFERENCE: 0652.2280001
CURRENT FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: US/09/899,569A
CURRENT FILING DATE: 2001-07-07
PRIOR APPLICATION NUMBER: DE 100 33 080.0
PRIOR APPLICATION NUMBER: DE 101 19 294.0
PRIOR APPLICATION NUMBER: US 60/243,158
PRIOR APPLICATION NUMBER: US 60/243,158
PRIOR APPLICATION NUMBER: US 60/243,158
PRIOR APPLICATION NUMBER: US 60/243,158
PRIOR APPLICATION NUMBER: US 60/247,747
PRIOR FILING DATE: 2001-10-25
PRIOR FILING DATE: 2001-06-14
NUMBER OF SEQ ID NOS: 40
SOFTWARE PAtentin Ver. 2.1
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APPLICANT: NO. US20020142003A1bert Schweifer
APPLICANT: Marwa Scherl-Mostageer
APPLICANT: Wolfgang Sommergruber
APPLICANT: Wolfgang Sommergruber
APPLICANT: Roger Abseher
TITLE OF INVENTION: Tumorassozilertes Antigen (
FILE REFERENCE: 0652.2280001
CURRENT APPLICATION NUMBER: US/09/899,569A
CURRENT FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: DE 100 33 080.0
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: DE 50/243,158
PRIOR APPLICATION NUMBER: US 60/243,158
PRIOR APPLICATION NUMBER: US 60/243,158
PRIOR APPLICATION NUMBER: US 60/247,747
PRIOR APPLICATION NUMBER: US 60/297,747
PRIOR TILING DATE: 2001-06-14
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.1
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Pred. No. 1.8e-292;
9; Mismatches 28;
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Sequence 48, Application US/09768826
Patent No. US20020012966A1
GENERAL INFORMATION:
APPLICANT: Shi et al.
TITLE OF INVENTION: 18 human secreted prote
FILE REFERENCE: PF512P1
CURRENT APPLICATION NUMBER: US/09/768,826
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: PCT/US00/22350
PRIOR FILING DATE: 2000-08-15

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vs-09-768-826-48
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PRICE SELLING DAMES AND BAPTON STORY SM: Homo Baptons
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                342 NKIYVVDLSNERAMSLTIEPRPVKOSRKFVPGCFV-CLESRTCSSNLTLTSGSKHKISFL 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 CTL----SIRDTRESDAGTYVECVERGNMKWNYKYDQLSVN-VTAS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 SRNIPVATNNPARAVOEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence 9, Application US/09972715
Patent NO. US20020110862A1
PATENAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             145 ODLLSRYRLEVPESVTV------QEGLCVSVPCSVLYPHYNWTASSPVYGSWEKEGADI 197
                                                                                                                                                                                                                                                                                                                                                                                                          447 SWKLLVPKDRLSLVLVPAQKLQOHTH------EKPCNTSFSYLVASAIPSODLYFGSF 498
                                                                                                                                                                                                                                                                                                                                                                 499 CPGGSIK--QIQVKQNISVTLRTFAPSFQ-----QEASROGLTVSFIPVFKEEG----- 545
                                                                                                                                                                                                                                                                                                                                                                                     198 PWDIPVATN-----TPSGKVQEDTHGRELLLGDPGTNNCSLSIRDARKGDSGKYYFQ-- 249
                                                                                                                                                                                                                                                                                                             309 WMGASVSSLDPTITRSSMLSLIPQPQDHG-TSLTCQVTLPGAGVTMTRAVRLNISYPPQN 367
                                                                                                                                                                                                                                                                                                                                               250 VERGSRKWNYIYDKLSVHVTALTHMPTESIPGTLESGHPRNLTCS-VPWACEQGTPPPTIT 308
                                                                                                                                                                                                                                                                                                                               546 -----VPTVTPD-TKSKVYLRTPN-WDRGLPSLT------SVSWNISVPRDQ 584
                                                                                                                                                                                                                                                                         368 LIMTVFQGDGTASTTLRNGSALSVLEGQSLHL--VCAVDSNPPARLSWTWGSLTLSPSQS 425
                                                                                                                                                                                                                                                                                          APPLICANT: FOUSSIAS, GEOTGE THE GENE APPLICANT: Diamandis, Eleftherios GENE TITLE OF INVENTION: NOVEL SIGLEC-LIKE GENE 11757 55USU1 US/09/972,715 FILE REFERENCE 11757 55USU1 US/09/972,715 CURRENT APPLICATION NUMBER
                                                                                                                                                                                                                                                         625 ----VLPKPSFH---HHSFWVNISNCSPTSGKQLDLLFSV--TLTPRTVDLTVILIAAVG 675
                                                                                                                                                                                                                                      426 SNLGVLELPRVHVKDEGEFTCRAQN--PLGSQHISLSLSLQNEYTGK#RPISGVTLGAFG 483
                                                                                                                                                                                                733 VYAVIEDTMYYGHLLODSSGSFLOPEVDTYRPFQGTMGVCPPSPPTICSRAPTAKLATEE 792
                                                                                                                       573 ARPOYPOECEAIGYEYSEIN 592
                                                                                                                                        793 PPPRSPPESESEPYTESHPN 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *12 Ta: 03: 29 2002
                                                                                                                                                                                                                    GG---VLLLSALGLIICCVKKKKKKTNKGPAVGIYNGNINTEMPROPKKFQKGRKDNDSH 732
                                                                                                                                                             ....DANAVRG---SASOGPLIESPADDSPPHHAPPALATPSPEE--GEIQYASUSFHK 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247; Indels 212; Gaps
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PRIOR APPLICATION NUMBER: US 60/239,006
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 15
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 477
TYPE: PRT
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US-09-972-715-9
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Best Local Similarity
Matches 103; Conserv
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                                                                                                                                                                                                       GENERAL INFORMATION: Wade
APPLICANT: Walke, Jaoming
APPLICANT: Scoville, John
APPLICANT: Scoville, John
APPLICANT: Scoville, John
APPLICANT: Scoville, John
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APPLICANT: Scoville, John
APPLICANT: Scoville, John
APPLICANT: JUSZA STORMANDER: USZ0020098491A1el Human Semaphorin Homologs and Poly,
APPLICANT: JUSZA STORMANDER: USZ0020098491A1el Human Semaphorin Homologs and Poly,
APPLICANT: JUSZA STORMANDER: USZ0020098491A1el Human Semaphorin Homologs and Poly,
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APPLICANT APPLICANT APPLICANT APPLI
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Patent No. US20020098491A1
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PRIOR APPLICATION NUMBER: US 60/208,893
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 47
LENGTH: 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192 MGASVSSLDPTTTRSSMLSLIPOPODHG-TSLTCQVTLPGAGVTMTRAVRLNISYPPQNL 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 WDIPVATN-----TPSGKVQEDTHGRFLLLGDPQTNNCSLSIRDARKGDSGKYYFQ--V 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251 TMTVFQGDGTASTTLRNGSALSVLEGQSLHL--VCAVDSNPPARLSWTWGSLTLSPSQSS 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 309 NLGVLELPRVHVKDEGEFTCRAQN--PLGSQHISLSLSLQNEYTGKMRPISGVTLGAFGG
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                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/205,274
PRIOR FILING DATE: 2000-05-18
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20.6%; Pred. No. 0.087;
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Db 258 DGSRRWGRYEGGVPEPRPGSCITDSLRS	403 DLTRLWMNVEKTISC-TDHRYCQRKSYSLQVPSDILHLPVELHDFSWKLLVPKD 455
	Query match 2.5%; Score 110; DB 10; Length 865; Best Local Similarity 19.9%; Pred. No. 0.51; Matches 108: Conservative 85; Mismatches 172; Indels 182; Gaps 27;
Query Match Best Local Similarity 18.6%; Pred Matches 93; Conservative 71; M	; TYPE: PRT ; ORGANISM: homo sapiens US-09-854-845-33
477	
NUMBER OF SEQ ID NOS: 50  NUMBER OF SEQ ID NOS: 50  SOFTWARE: PastSEQ for Windows Version Second No. 43  SEQ ID NO. 43  LENGTH: 744	PRIOR APPLICATION NUMBER: US 60/205,274 PRIOR FILING DATE: 2000-05-18 PRIOR APPLICATION NUMBER: US 60/208,893 PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 2000-06-02  PRIOR ENTLING DATE: 2000-06-02  PRIOR ETIING DATE: 2000-06-02	FILE REFERENCE: LEX-0177-USA CURRENT APPLICATION UNUMBER: US/09/854,845 CURRENT FILING DATE: 2001-05-14
; FILE REFERENCE: LEX-01/7-USA ; CURRENT APPLICATION NUMBER: US/09/85 ; CURRENT FILING DATE: 2001-05-14 ; CURRENT FILING DATE: 400/205	APPLICANT: Scoville, John APPLICANT: Turner, C. Alexander Jr. TITLE OF INVENTION: No. US20020098491Alel Human Semaphorin Homologs and Polynucleotid
; APPLICANT: Scoville, John ; APPLICANT: Turner, C. Alexander Ji ; TITLE OF INVENTION: No. US20020098	GENERAL INFORMATION: APPLICANT: Walke, D. Wade APPLICANT: Walke, D. Wade APPLICANT: Walke, D. Wade
<pre>Sequence 43, Application US/U9834843 ; Patent No. US20020098491A1 ; GENERAL INFORMATION:    APPLICANT: Walke, D. Wade ; APPLICANT: Wang, Xiaoming</pre>	RESULT 8 US-09-854-845-33 ; Sequence 33, Application US/09854845 ; Patent No. US20020098491A1
8	760 PWSFS
Db 859 PWSrS 863	802
802 ESE	EVRLHHSPPLPSCVALVNQPPHS
Db 800 ASG-LGVPSQLPHPIWSSSPAPCGDLFVK	657 ETRQVLCQPPKPCVHSHAI
Ä	TEMPROPKKFQKGRKDNDSHVYAVIEDTMVYGHLLQDSSGSFLQPEVDTYRP
Qy 713TEMPKQYKKEQKGKKUNUSHYIAYIBU  13	597
546	686
686	Oy 649KOLDLLESVTLTPRTVDTVILIAAVGGVVLLISALG 685  1   1   1   1   1   1   1   1   1   1
Qy 649KQLDLLFSVTLTPRTVD :   : : :     Db 636 ENGLRTLLASYSLTVRPATPAPAPKAPAT	   SGNYGCYAE
576 RG	427
620	Qy 563 NWDRGLPSLTSVSWNISVPRDQVACLTFFKERSGVVCQTGRAFMIQEQRTRAEEIF 619
Qy 563 NWDRGLPSLTSVSWNISVPRDQVACL'	Qy 516 TLRTFAPSFQQEASRQCLTVSFIPYFKEEGVFTVTPDIKSKVILKTF- 362
Db 468 IEETQVFRESQSVENLVISLLQHSLYV	GRPLLLKRNIRYTHLTGTPVTTPAGPTYDLLFLGTADGWIHKAVVLGSGMHI
516	QY 456 RLSLVLVPAQKLQQHTHEKPCNTSFSYLVASAIPSQDLYFGSECPGGSIKQIQVKQNISV 515
Qy 456 RLSLVLVPAQKLQQHTHEKPCNTSFSYLV/  :  ::   :::  Db 416 GRPLLLKRNIRYTHLTGTPVT	Qy 403 DIRRIMMNVEKTISC-TDHRYCQRKSYLQVESDLIHDEVELDESWELLVERU 455    1
Db 357 DGSRRWGRYEGGVPEPRPGSCITDSLRSQ	Matches 109; Conservative 85; Mismatches 172; Indels 182; Ga

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YCQRKSYSLQVPSDILHLPVELHDFSWKLLVPKD 455
                                                           ore 108.5; DB 10; Length 744; ed. No. 0.54; Mismatches 160; Indels 177; Gaps
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RSQGYNSSQDLPSLVLDF-VKLHPLMARPVVPTR 316
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;QGYNSSQDLPSLVLDF-VKLHPLMARPVVPTR 415
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; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-27
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US-09-854-845-27
Sequence 27, Application US/09854845
Patent No. US20020098491A1
GENERAL INFORMATION:
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APPLICANT: Walke, D. Wade
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APPLICANT: Walke, D. Wade
APPLICANT: Walke, D. Wale
APPLICANT: Walker, D. Wale
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: NO. US20020098491A1e1 Human Semaphorin Homologs and Polynuclec
FILE REFERENCE: LEX-0177-USA
CURRENT APPLICATION NUMBER: US/09/854,845
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: US 60/205,274
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2000-06-02
SUSTUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 27
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468 IEET--QVFRESQSVENLVISLIQHSLYVGAPSGVIQLPLSSCSRYRSCYDCILARDPYC 525
                                     516 TLRTFAPSFQQEASRQGLTVSFIPYF----KEEGVFTVTPDTKSK------VYLRTP-- 562
                                                                             416 GRPLLL---KRNIRYTH-----LTGTPVTTPAGPTYDLLFLGTADGWIHKAVVLGSGMHI 467
                                                                                                              456 RLSLVLVPAQKLQQHTHEKPCNTSFSYLVASAIPSQDLYFGSFCPGGSIKQIQVKQNISV 515
                                                                                                                                                        357 DGSRRWGRYEGGVPEPRPGSCITDSLRSQGYNSSQDLPSLVLDF-VKLHPLMARPVVPTR 415
                                                                                                                                                                                     403 DLTRIAMNUVEKTI-----SC-TDHRYCQRKSYSLQVPSDILHLPVELHDFSWKLLVPKD 455
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	QVACLTFF	.PSFQQEASRQGLTVSFIPYFKEEGVFTVTPDTKSKVYLRTP     :   :   :	RLSLVLVPAQKLQQHTHEKPCNTSFSYLVASAIPSQDLYFGSFCPGGSIKQIQVKQNISV  :  :: :	DLTRLWMNVEKTISC-TDHRYCQRKSYSLQVPSDILHLPVELHDFSWKLLVPKD 	Score 108; DB Pred. No. 0.59; 73; Mismatches	on US/09854845  91A1  Jahn  John  Alexander Jr.  Alexander Jr.  US20020098491A1e1 Human  177-USA  WEDER: US/09/854,845  2001-05-14  2001-05-14  10-05-18  DER: US 60/205,274  10-05-18  DER: US 60/208,893  50  Windows Version 4.0	PESE 802   :  PPAE 781	YRPFQGTMGVCPPSPPT 	CCVKKKKKKTNKGPAVGIYNGNINTEMPRQPKKFQKGRKDNDSHVYAVIEDTMVYGHLLQ 	 PKAPATPGAQLAPDVR	LNGSMGLSDGQGGYRVGVD	303 NUNGLESLISVSWNISVPROQVACLTEFKERSGVVCQTGRAFMIIQEQRTRAEEIFSLD       : :   :           :   :
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A;Title: The intrinsic factor-vitamin Bl2 receptor and target of teratogenic antiboda A; Reference number: Z16459; MUID:98148073; PMID:9478979
A; Accession: T08618
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 02-Aug-2002
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                                                                                                                                                                                                                                                                                                                  127 WDVKAHKSIGLELQFSIPRLRQIGPGESCPDGVT----HSISGRIDATVVRIGTFCSNGT 182
                                                                                                                                                                                                                                                  183 VSRIKMQEGVKMALHLPWFHPRNVSGFSIANRSSIKRLCIIESVFEGE---GSATLMSAN
                                                                                                                                                                                                                                                                                                                                                                                  70 IKSGERIVFTFSCQSPENHFVIEIQKNIDCMSGPCPFGEVQLQPSTS--LLPTLNRTFI- 126
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                                                                                                                                                                                                                                                                                   WFIRGLPGHYLTLSFEDFNL-QSSPG--CTKDFVEIWENHTSGRV-----LGRYCGNST
                                                 PGI-----LRLQFQVLVQHPQNESNKIYVVDLSNERAMSLTIEPRPVKQSRKFVPG
                                                                                  SRVNVTNEFKSSGNTMK-VVFFTDGSRPYGGFTASYTSTEDAVCGGFLPSVSG--GNFSS
                                                                                                                 ERKEERVEYYIPGSTTNPEVFKLEDKQP------
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Pred. No. 0.72;
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polyketide synthas
probable NADPH cyt
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T08618
T33135
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Gaps

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Minimum DB

seq length: 0 seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 10

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Listing

Database

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QYWILADLEKSDDVESPNYPIQPNPQKFLFDTEPAELLITAFNSGNELVTSSTLLKI 545 NLSNCERKEERVEYYIPGSTINPEVFKLEDKQPGNMAGNFNLSLQGCDQDAQSP 323 :   :	LCIIESVFEGEGSATLMSANYPEGFPEDELMTWQFVVPAHLRASVSFLNF 2	VTHSISGRIDATVVRIGTFCSNGTVSRIKMQEGVKMALHLPWFHPRNVSGFSIANRSSIK 218 :	WDVKAHKSIGLELQFSIPR	<pre>Match 2.8%; Score 123.5; DB 2; Length 986; Ocal Similarity 18.3%; Pred. No. 1.1; s 128; Conservative 102; Mismatches 242; Indels 229; Gaps 32;</pre>	CESP:C45G7.5 osition: 4 ns: 373/3; 466/1; 524/3; 559/3; 722/2; 776/3; 839/2; 969/2 family: Caenorhabditis elegans hypothetical protein C45G7.5	.;Residues: 1-986 <dan> ;Cross-references: EMBL.AF067611; PIDN:AAC19183.1; GSPDB:GN00022; CESP:C45G7.5 ;Experimental source: strain Bristol N2; clone C45G7 ;Genetics:</dan>	;Kolecule type: DNA	4.; Wamsley, P. to the EMBL Data Library, May 1998 tion: The sequence of C. elegans cosmid C45G7. se number: z21288	193139 hypothetical protein C45G7.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000 C;Accession: T33135		LDLLESVTLTPRTVDLTVIL 670 : :	FUCKNESSIFE	NWNCTYLIDADPOSIVIITEVSEHLEDRSATTGTCDHDGIHI-IKGRNISSTDI.	HHSFWVNISNCSPTSGKO 650	TLLATSCGDVAPSPIVTSGNIFTAVFQSEEMAAQGFSASFISRCGRTFNTSPGDIISPNF 2936	KSPHWPQTFPENSRCSWTVITHESKHWEISFDSNFRIPSSDSQCQNSFVKVWEGRLMINK 2876	RTPNWDRGLPSLTSVSW	PIQSGSNQLIVTENT NNQGQTRGEVATWITNALGCGGTEHSANGTI 2816	QIQVKQN-ISVTLRTFAPSFQQEASRQGLTVSFIPYFKEEGVFTVTPDTKSKVYL 559	CSWLLKAPEGHTITLTESDELLEAHPTCTSDSVTVRNGDSPGSPVIGRYCGQSVPR 2770	-SWKLLVPKDRLSLVLVPAQKLQQHTHEKPCNTSFSYLVASAIPSQDLYFGSFCPGGSIK 505	TAPLVIPYPQVWIHFVSNERVEYTGFYIEYSFTDCGGIRTGDNGVISSPNYPNLYSAWTH 2714	SDILHLP VELHDF 446	CFVCLESRTCSSNLTLTSGSKHKISFLCDDLTRLWMNVEKTISCTDHRYCQRKSYSLQVP 433

A;Reference number: A92706; MUID:88115411; PMID:2963004
A;Accession: A25908
A;Molecule type: mRNA
A;Recession: A25908
A;Molecule type: mRNA
A;Residues: 1-2499 <LOB>
A;Cross-references: GB.303527; NID:g162873; PIDN:AAA30455.1; PID:g162874; GB:M15869
A;Cross-references: GB.401, 1089
A;Cross-references: GB.401, 1089
A;Clickman, J.N.; Conibear, E.; Pearse, B.M.F.
EMBO J. 8, 1041-1047, 1989
A;Title: Specificity of binding of clathrin adaptors to signals on the mannose-6-phos A;Ritle: Specificity of binding of clathrin adaptors to signals on the mannose-6-phos A;Contents: annotation; HA-II adaptor binding
C;Comment: This protein binds phosphorylated lysosomal enzymes and insulin-like growt C;Comment: This protein binds phosphorylated lysosomal enzymes and insulin-like growt C;Superfamily: mannose 6-phosphate receptor, cation-independent; fibronectin type II C;Keywords: Golgi apparatus; membrane protein
C;Keywords: Golgi apparatus; membrane protein
F;1912-1951/Domain: HA-II adaptor binding mannose 6-phosphate receptor protein, cation-independent - bovine C:Species: Bos prinigenius taurus (cattle) C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999 (C:Accession: A25908; A30788; S09404 R:Lobel, P.; Dahms, N.M.; Kornfeld, S. Ricbel, P.; Dahms, N.M.; Kornfeld, S. J. Biol. Chem. 263, 2563-2570, 1988 A;Title: Cloning and sequence analysis of the cation-independent mannose 6-phosphate A;Reference number: A92706; MUID:88115411; PMID:2963004 RESULT A30788

Matches Query Match
Best Local Similarity Conservative 2.7%; Score 118; DB 1; I 19.9%; Pred. No. 11; htive 100; Mismatches 343; DB 1; Length 2499; Indels 340;

Gaps

56;

QΥ Вb Ş Вþ Ş 1760 ---LADRHFNYTSL-----ITFHCKRGVSMGTPKLLRTSVCDFVFEWETPLVCPDEVK 1809 1710 MHGLACPAGTAVCKVPVDGP------PIDIGRVAGPPILNPIANEVYLNFESSTPC 1759 101 57 1 MAGINCGVSIALLGVLLLGAARLPRGAEAFEIALPRESNITVLIKLGTPTLL----AKPC SGPCPFGEVQLQPSTSLLPTLNRTFIWDVKAHK-SIGLELQFSIPRLRQIGPGE-SCPDG 158 YIVISKRHITMLSIKSGERIVETTESCQ-----SPE-----NHEVIEIQKNIDC----M 100 56

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intrinsic factor-B12 receptor Cubilin precursor - human
(;Speckes: Homo sapiens (man)
(;Speckes: Homo sapiens (man)
(;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Aug-2002
(;Accession: T09456
G;Accession: T09456
G;Kozyvaki, R.; Kristiansen, M.; Silahtaroglu, A.; Hansen, C.; Jacobsen, C.;
Blood 91, 3593-3600, 1998
A;Title: The human intrinsic factor-vitamin B12 receptor, cubilin: Molecular
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A;Reference number: Z16677; MUID:98241400; PMID:9572993
A;Accession: T09456
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Molecule type: mRNA
A; Residues: 1-3623 <KNOZ>
A; Residues: 1-3623 <KNOZ>
A; Cross-references: EMBL: AF034611; NID: g3929528; PIDN: AAC82612.1; P
A; Gross-references: EMBL: AF034611; NID: g3929528; PIDN: AAC82612.1; P
C; Genetics:
A; Map position: 10p12
C; Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology
C; Keywords: receptor; vitamin B12 uptake
F; 1-24/Domain: signal sequence #status predicted <SIG>
F; 25-3623/Product: intrinsic factor-B12 receptor #status predicted
F; 436-467/Domain: EGF homology <EGF>
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                                                                                                                                                                                                                                                                                                                                                CLTF--FKERSGVVC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FVTNERVEHIGFHAKY-------SFTDCGGIQ-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --THEKPCNTSF--SYLVASAIPSQDLYFGSFCPGGSIKQIQVKQNISVTLRTFAPSFQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APEGRRITLMFNNLRLATHPSC--NNEHVIVFNGIRSNSPQLEKLCSSVNVSNEIKSSGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -------LGRYCGNTIPDSIDTSSNTAVVR---FVTDGSVT------
LSVVLLTFVSFHLEARSAVTGSCVNDGVHIIRGYSVMSTPFATVCGDEMPAPLTI 3009
                                                                                                                -KTNKGPAVGIY---
                                                                                                                                                    SFDNNFLIPSGDGQCQNSFVKVWAGTEEVDKALLATGCGNV----APGPVITPSNTFTAV
                                                                                                                                                                                                                              SLQGGGFYATWNTQTLGCGGIFHSDNGTIRSP--HWPQNFPENSRCSWTAITHKSKHLEI
                                                                                                                                                                                                                                                                                                        TLTFSDFDIEPHTTCAWDSVTVRNGGSPESPIIGQYCGNSNPRTIQSGSNQLVVTFNSDH
                                                                                                                                                                                                                                                                                                                                                                                                                          EASRQGLTVSFIPYFKEEGVFTVTPDTKSKVYLRTPNWDRGLPSLTSVSWNISVPRDQVA
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                                                                          FQSQEAPAQGFSASFVSRCGSNFTGPSGYIIS--PNYPKQY----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                  -TMVYGHLLQDS---SGSFLQPEVDTYR-----PFQGTMGVCPPSPPTI
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                                                                                                                                                                                                                                                                    -QEQRTRAEEIFSLDEDVLPKPSFHHHSFWVNISNCSPTS----GKQLDL
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                                                                                                          -----NGNINTEMPRQPKKFQKGRKDNDSHVYAVIED--
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Pred. No. 20;
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                                                                          -DNNMNCTYVIEANP
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RESULT

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R;Finelli, A.L.; Xie, T.; Bossie, C.A.; Blackman, R.K.; Padget Genetics 141, 271-281, 1995

A;Fittle: The tolkin gene is a tolloid/BMP-1 homologue that is A;Reference number: S58984; MUID:96042912; PMID:8536976

A;Accession: S58984
hypothetical protein T01G9.3 - Caenorhabditis C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 *sequence_revision 15-Oct-C;Accession: T24315 R;Lennard, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;529-722/Domain: astacin homology <AST>
F;958-993/Domain: EGF homology <EGF>
F;1118-1153/Domain: EGF homology <EGF1>
F;614,618,624,673/Binding site: zinc (His, His, F;615/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: tolkin
A;Cross-references: FlyBase:FBgn0004885
C;Superfamily: astacin homology: EGF homology
C;Superfamily: astacin homology: zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Drosophila melanogaster
C;Date: 19-Jul-1996 #sequence_revision 26-Jul-1996
C;Accession: S58984
R;Finelli, A.L.; Xie, T.; Bossie, C.A.; Blackman, F
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A; Residues: 1-1464 <FIN>
A; Residues: 1-1464 <FIN>
A; Cross-references: EMBL: U34777; NID: 91002985; PIDN: AAC47015.1;
A; Note: the authors did not translate the codon for residue 722
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Best Local
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                                                                                                                                                                                                                            VASAIPSQDLYFGSFCPGGSIKQIQVK 510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PNGTI-TSPSFPEMYPLLKECIWEIVAPPKHRISLNFTHFDL------EGTAHQQS 1052
                                                                                                                                                                                                                                                                  QYCGNVLPQDINSMTHSLLVRFKTDGSVPMKGFSASYVAVPNSGEYDHSDEDVENSYSSE 1411
                                                                                                                                                                                                                                                                                                                                                DD----GMDCEWTIAAPDNSYVQLIFLTFDIESSENCTFDYVQVFSDIDDVYGQYGPMYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLSNERAMSLTIEPRPVKQSRKFVPGCFVCLESRTCSSNLTLTSGSKHKISFL-----C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VFKLEDKQPGNMAGNENLSLQGCDQDAQSPGIL----RLQFQVLVQHPQNESNKIYVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FSPNYPDSYPPNADCVWHFITTPGH-RIKLIFNEFDVESHQECTYDNVAVY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MSANYPEGFPEDELMTWQFV-VPAHLRASVSFLNFNL-SNCERKEERVEYYIPGSTTNPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DCGYDSVTVYSKLGENRLKRIGTFCGSSIPPTATSESN---ALRLEFHSDKSIQRSGFAA 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                      --LPVELHDESWKLL------VPKDRLSLVLVPAQKLQQHTH-EKPCNTSFSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                              LKTDKNKQKNGFTASHSTACGGYLRATSQVQQFYSHARFGNQDY 1295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----DGESESSVLGRFCGDKIPFPI----SSTSNQMYMV
                                                                                                                                                                                      GSLKSIYIE
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Pred. No. 5.
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                                          15-Oct-1999 #text_change 15-Oct-1999
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zonadhesin - pig
cynachesin - pig
cyspecies: Sus scrofa domestica (domestic pig)
Cynate: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
Cynaccession: T34022
R;Hardy, D.M.; Garbers, D.L.
                                                                                     RESULT
T34022
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A;Gene: CESP:T01G9.3
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A; Introns: 68/3; 346/1;
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A;Experimental source: clone
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                                                                                                                                                                                                                                                          MPRQPKKFQKGRKDNDSHVYAVIEDTMVYGHLLQDSSGSF----LQPEVDTY----RPFQG
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19.9%;
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44;

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RESULT 8
T19173
hypothetical protein C05D12.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_c
C;Accession: T19173
R;Coles, L.
submitted to the EMBL Data Library, August 1995
A;Reference number: 219084
A;Accession: T19173
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1027 <WIL>
A;Cross-references: EMBL:Z50872; pIDN:CAA90754.1; GSPDB:GN
A;Cross-references: EMBL:Z50872; piDN:CAA90754.1; GSPDB:GN
A;Experimental source: clone C05D12
C;Genetics:
A;Gene: CESP:C05D12.2
A;Map position: 2
A;Introns: 20/1; 55/2; 128/3; 241/3; 333/1; 352/3; 406/1;
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C; Genetics;
A; Gene: Zan
C; Function;
A; Description:
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A;Title: A sperm membrane protein that binds in a species-specific A;Reference number: 221464; MUID:96064658; PMID:7592795
A;Accession: T34022
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2476 <HAR>
A;Cross-references: EMBL:U40024; NID:g1066465; PID:g1066466; PIDN:A
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                                                      99
env polyprotein - avian reticuloendotheliosis vi.
N.Alternate names: coat polyprotein
N.Contains: coat protein gp23
C.Species: avian reticuloendotheliosis virus
C.Date: 28-Aug-1985 #sequence_revision 28-Aug-198
C.Accession: A03999
R.Wilhelmsen, K.C.; Eggleton, K.; Temin, H.M.
J. Virol. 52, 172-182, 1984
A.Fitle: Nucleotide acid sequences of the oncogen
A.Reference number: A93003; MUID:85009850; PMID:87MOLECULE type: DNA
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                                   sequences of the oncogene v-rel
)3; MUID:85009850; PMID:6090694
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A; Gene: env
C; Superfamil
C; Keywords:
                                                                                                                                      A;Cross-references: SGD:S0001198
A;Map position: BR
C;Superfamily: nlarvary
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$46754
hypothetical protein YHR155w - yeast (Saccharomyces cerevisiae)
hypothetical protein YHR155w - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change
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A;Experimental source: strain A
A;Experimental source: strain A
A;Note: strain A is a helper virus of the strain T
C;Comment: Enzymatic cleavages of env polyprotein may yield mature proteins including C;Genetics:
                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, June 1994 A; Description: The sequence of S. cerevisiae A; Reference number: S46752
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R; Macri, C.
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A;Residues: 1-1228 <MAC>
A;Cross-references: EMBL:U10397; NID:g500647; PID:g500650; GSPDB:GN00008; MIPS:YHR155w
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Best Local
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                                 SNGTVSRIKMQEGVKMALHLPWFHPRNVSGFSIANRSSIKRLCIIES----VFEGEGSAT
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     SNGNNSEEKGLSG-
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                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                             #sequence_revision 28-Oct-1994 #text_change 19-Apr-2002
                                                                                  2.6%;
                                                                                                                                      repeat homology
WLYMKTTVGHDPKRVVWVRRWCFLQNNVFGVFSLSPSKT
                                                                    85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60; Mismatches
                                                                                  Score 114; DB Pred. No. 7.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 115; DB 1;
Pred. No. 2.1;
                                                                    Mismatches
                                                                                                                                                                                                                                                                                                           cosmid
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                                                                    196;
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                                                                                                      Length 1228;
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                                                                                    399
                                                                                                                                                                                                                         284 RAMVWNVETGESLG-----SFPRSGNWYTKSSWCPSNSNRVAVASLEGKVSIFSIQSTNT 338
                                                 256 VPAHLRAS-----VSFLNFNLSNCERKEERVEYYIPGSTTNPEVFKLEDKOPGNMAGN
                 MAVSKRASRSKFAELLGYKTLKPKNDEDDSKVDESVAKDSTTPNELSK---
                                                                                    S-PNSKEVTITSAPDEVEQDEAKSFHSSAKFQTEKEITDFCQKGVEESASEEEAINWKLL
                                                                                                                    SIANRSSIKRLCIIESVFEGEGSATLMSANY-----
                                                                                                                                                     DKSQEASIKGATSIDDNEFFNNLPSIAGSQEPSFSLPLAPKWFKVPVGARFGFPNKIVSF
                                                                                                                                                                                                                                                        RTFIWDVKAHKSIGLELQFSIPRLRQIGPGES-CPDG----VTHSISGRID-----
                                                                                                                                                                                     -----ATVVRIGTECSNGTVSRIKMQEGVKMALHLPWE------HPRNVSGF
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		SULT 11	CO.
	VLEIFQELDEBIENEKKIIKDNLSESEH-YSKDYDYLLKSTYDHH 752	709	
	587 CLTFFKERSGVVCQTGRAFMIIQEQRTRAEEIFSLDEDVLPKPSFHHH 634	587	
80'	YDKSPKHVSSRMLHMQRGDGLRENMSVFFTDRRAVASKLQFLIENKAMHIPKGEKE 708	653	
586	YLRTPPRDRGLPSLTSVSWNISVPRDQVA 5	558	
52	LQVPKEL-VLLRYSSVWCPNNKQKFASMAFVTLNHIYVYLNISGFSYLRRIDLLDIDSIE 652	594	
557	IQVKQNISVTLRTEAPSFQQE-ASRQGLTVSFIPYFKEEGVFTVTPDTKSKV	507	
93	NDLSYLVNPLKGSSVHKPATVSNSSRFSVSYPDYYPYSLKVDDIQFRSIFFSVNHDF 593	537	
506	DRISLVLVPAQKLQQHTHEKPCNTSFSYLVASAIPSQDLYFGSFCPGGSIKQ	455	
536	EDDIYSIIDNKAYHLRVISTPIATQLTHLALFSTELSVSNYYPCATQANTWGTANW	481	
454	VEKTISCTDHRYCQRKSYSLQVPSDILHLPVELHDFSWKLLVPK	411	
480	IALSIKEENDPRYQLARKKIEPQFFEFASSSSTSTDKLLTSFSSKTLT-LVEELKKNYMS	422	
410	MSLTIEPRPVKQSRKFVPGCFVCLESRTCSSNLTLTSGSKHKISFLCDDLTRLWMN 4	355	
421	KEPRNECFKLRIQNPNCKTEEENTYIDIILQAESIDELKSWINTLTSHKR 4	372	
354	FKLEDKQPGNWAGNFNLSLQGCDQDAQSPGILRLQFQVLVQHPQNESNKIYVVDLSNERA	295	
371	YVEETDKFGILWITV	353	
94	LMSANYPEGFPEDELMTWQFYVPAHLRASVSFLNFNLSNCERKEERVEYYIPGSTTNPEV 294	235	

C;Genetics:
A;Gene: SPDB:SPBC8D2.20c
A;Map position: 2 A; Nolecule type: DNA A; Molecule type: DNA A; Residues: 1-1224 < LYN> A; Cross references: EMBL, ALO22072; PIDN: CAA17835.1; A; Cross references: strain 972h-; cosmid c8D2 R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Lauber, J.; Hilbert, submitted to the EMBL Data Library, March 1998
A;Reference number: Z21948
A;Accession: T40765 webl protein homolog - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999
C;Accession: T40765
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Lauber, J.; Hilbert, H.; Duest A; Experimental source: strain C; Genetics: A; Status: preliminary; translated Query Match
Best Local Similarity 17.9: 2.6%; Score 113; 17.9%; Pred. No. 9; from GB/EMBL/DDBJ DB <u>ب</u> GSPDB:GN00067; SPDB:SPBC8D2.20c Length 1224; H.; Duesterhoeft,

108;

Mismatches

372;

Indels

222;

Gaps

32;

168

---PEGFPEDELMTWQFV 255

457

505

398

249	98 LPWFHPRNVSGFSIANRSSIKRLCIIESVFEGEGSATLMSANYPEGFPEDEL    :      :: : :: :   : :	Oy 19
33;	/ Match 2.6%; Score 113; DB 2; Length 3329; Local Similarity 18.8%; Pred. No. 41; Nes 125; Conservative 94; Mismatches 226; Indels 220; Gaps	Query M Best Lo Matches
	BRCA2 family: breast cancer tumor suppressor BRCA2	A;Gene: C;Superf
7.1	A;Residues: 1-3329 <mca> A;Cross-references: EMBL:U89652; NID:g2443438; PID:g2443439; PIDN:AAB7137 A;Experimental source: strain CD1; 129SV; ICR Swiss</mca>	A; Residues: A; Cross-reforment A; Experiment
	T4220 elimina ype: mi	A; Accession: A; Status: pro A; Molecule t;
2 breast cancer	n: Characterization of the mouse number: 222073	A; Referen
ee, H.; Futreal	K.A.; Haugen-Strano, A	R; McAlli
000	susceptibility protein BRCA2 - mouse musculus (house mouse) -1999	breast cancer C; Species: Mus C; Date: 03-Dec
	12	RESULT 1
	48 PSVTPQLPPVSSRLP 1062	Db 1048
	818 SKDT-DIPLLNTQEP 831	Qy . 81
47	999TYKPHGGSQIVPPPKQPANRVVPLPPTASQRASAYEPPTVSVPSPSALS 104	Db 99
7	58 EVDTYRPFQGTMGVCPPSPPTICSRAPTAKLATEEPPPRSPPESESEPYTFSHPNNGDVS 817	Qy 75
æ ·	TPVAPQSPVAAASRISSSPNMPPSNPYTPIAVASSTVNPAH	9
7	TNKGPAVGIYNGNINTEMPROPKKFOKGRKDNDSHVVAVTEDTMVVGHIIODSSGSETOP	
7	MSRTSSVSTLPPPPPTASMTASAPAIASPP	
	AFMLGQLFMKKAAFSMAFVKSFFFGASSAQFAA	
. 7	TRACEIFSLDEDVLPKPSEHHHSEWVNISNCSPTS	Oy 61
37	778 EFPGAKEEIQRLTMLLEPHAVPPIHQIKQTGYAPVQPKTSQASSILPTVPRTTSYTSPYA 8	Db 77
ίλ	577 NISVPRDQVACLTFFKERSGVVCQTGRAFMIIQEQR 612	Оу 57
7	720 MDKVSMFRSIVVYKDDELSATKDWKLAGLYEVYIAYAKILSASGKFDDAMSYLNLVPT 777	Db 72
<b>с</b> ъ	529 -SRQGLTVSFIPYEKEEGVETVTPDTKSKVYLRTPNWDRGLPSLTSVSW 576	Оу 52
<b>.</b>	669 EKSIRSAEFCYIASKSLQSYANLW	Db 66
28	473 EKPCNTS-FSYLVASAIPS-QDLYFGSFCPGGSIKQIQVKQNISVTLRTFAPSFQQEA 5	Qy 47
8	609 KPSYMRLSACIADNDLQNVVDNAEVSEWKDIFVFICTYATDDEFAPLCSTLGQRLEDLED 66	Db 60
	421 RYCQRKSYSLQVPSDILHLPVELHDFSWKLLVPKDRLSLVLVPAQKLQQHTH 472	Qy 42
<u> </u>	565 GDVLSAVKACLEEKKISEALFLSTEGGKECRKCVRDAFYELQEH 608	Db 565
<b>4</b>	- NANNENYDDDSSFYGKLAESVOEVSIADKKDAETYKDSFKIFNDEDSDLEKNTTEALLT	
_	301 FNISTORCEDADADADATION OF THE PROPERTY OF T	30

					ncer	real																						
)		A; Gene	A; Re	A; St	A; Ti	R; Co	C; Da	RESULT T30904 breast	DЬ	Qy	Db	Qy	B 5	מט	ş Ş	В	Qγ	문 5	9 5	ş 8	망	ОУ	망	Qy	문 :	Ş	망	Qy
Keywords		Gene: B	sidue	A; Status:   A; Molecule	tle: feren cessi	Mol.	te: 2 cessi	LT 13 St ca St ca	1710	776	1651	728	1612	100/	612	1523	553	1472	7 L	1449	1373	412	1335	353	1295	297	1243	250
	addatasat	2 t Cancer timor	A;Residues: 1-3329 <con> A;Cross-references: EMBL:U82270; NID:g1854950; PID:g1854951; PIDN:AAB48306.1</con>	Status: preliminary; translated from GB/EMBL/DDBJ Molecule type: mRNA	A:Title: Cloning, chromosomal mapping and expression pattern of the mouse Brca2 gene A;Reference number: 220931; MUID:97217789; PMID:9063750 A:Accession: T30904	<pre>stratton, M.; Dixon, A.; Campbell, E.; Tal</pre>	C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jan-2000 C;Accession: T30904	ncer tumor suppressor Brca2 - mouse	DPNVC 1714	PPTIC 780	WLREQGDKLGTRNTIKIECVKEHTEDFAGNASYEHSLVIIRTEIDTNHVSENQVSTL-LS 1709		VILLHAYVGGVULLUSAKGLI (CVNRKKRIYRIGFAYVI INSKRIVERKE (PRAFKY (AK. 1878)   1   1   1   1   1   1   1   1   1	ASKCEEMONE VURETEMERQONE HMERQTENERTUNGTSSKVQENEENNVERNYR	RTRAEEIFSLDEDVLPKPSFHHHSFWVNISNCSPTSGK-QLDLLFSVTLTPRTVDLT	TQYVRKTASFSQGSKPL	TKSKVYLR-TPNWDRGLPSLTSVSWNISVPRDQVACLTFFK	TVTVSQLPAQQHPEYEIESTKEPTLLSFHTASGKKVKIMQESLDKVKNLFDE	COUNTREANDS SAGADI SAGAM ISOCOSOGADO CERCO TENOS TOTO TOTO TOTO TOTO TOTO TOTO TOTO T	KLLVPKDRL-SLVLVPAQKLQQHTHEKPCNTSFSYLVASAIPSQDLYFGSFCPG 501 . KLLVPKDRL-SLVLVPAQKLQQHTHEKPCNTSFSYLVASAIPSQDLYFGSFCPG 501 .	EET-	EKTISCTDH	PADQGSKCPESCTQYAREENTQ-IKENISDLTCLEIMKA 1372	RAMSLTIEPRPVKQSRKFVPGCFVCLESRTCSSNLTLTSGSKHKISFLCDDLTRL-WMNV 411	KNTKHEDSYTSSQRNNLENSDGSMSSTSGPYXIHKGDSDL	T.E.D.E.O.C. T. T. AND ENOUGHON TO DESCRIPTION OF THE TRANSPORTED TO T	AHHDSVASVFKIKKONTEKSFDEKSSKCOVTLONNIEMTTCIFVG	MTWQFVVPAHLRASVSFLNFNLSNCERKEERVEYYIPGSTTNPEVFK 296

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RESULT 14
A39613
Oligodendrocyte-myelin glycoprotein precursor - human
C:Species: Homo sapiens (man)
C:Date: 13-Sep-1991 #sequence_revision 03-Oct-1995 #text_change 31-Jan-2000
C:Date: 13-Sep-1991 #sequence_revision 03-Oct-1995 #text_change 31-Jan-2000
C:Accession: A36688; A34210; A39613; A30187
R:Mikol, D.D.; Alexakos, M.J.; Bayley, C.A.; Lemons, R.S.; Le Beau, M.M.; Stefar
J. Cell Biol. 111, 2673-2679, 1990
A:Tille: Structure and chromosomal localization of the gene for the oligodendroc
A:Reference number: A36688; MUID:91115958; PMID:2277079
A:Accession: A36688
A:Molecule type: DNA
A:Residues: 1-440 <MII>
A:Cross-references: GB:X57436; NID:923105; PIDN:CAA40684.1; PID:923106
R:Mikol, D.D.; Gulcher, J.R.; Stefansson, K.
J. Cell Biol. 110, 471-479, 1990
A:Title: The oligodendrocyte-myelin glycoprotein belongs to a distinct family of A:Maccession: A34210; MUID:90130636; PMID:1688857
A:Accession: A34210; MUID:90130636; PMID:1688857
                                                      A; Molecule type: DNA
A; Residues: 8-20, 'X', 22-440 <MI2>
A; Residues: 8-20, 'X', 22-440 <MI2>
A; Cross-references: GB: X51694; NID: g35144; PIDN: CAA35991.1; PID: g35145
R; Viskochil, D.; Cawthon, R.; O'Connell, P.; Xu, G.; Stevens, J.; Culve
Mol. Cell. Biol. 11, 906-912, 1991
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A; Reference number: A39613; MUID:91117257; A; Accession: A39613
                                      Mol. Cell. Biol. 11, 906-912, 1991
A;Title: The gene encoding the oligodendrocyte-myelin glycoprotein is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RTRAEEI - - - FSLDEDVLPKPSFHHHSFWVNISNCSPTSGK - QLDLLFSVTLTPRTVDLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TQ---YVRKTASFSQGSKPL-----KDSKKELTLAYEK-----IEVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VTVSQLPAQQH---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RETDELTVISDSLNSKILHGINKDKMHTSCHKK-----AISIKKVFEDHF-PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----KLLVPKDRL-SLVLVPAQKLQQHT--HEKPCNTSFSYLVASAIPSQDLYFGSFCPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RAMSLTIEPRPVKQSRKFVPGCFVCLESRTCSSNLTLTSGSKHKISFLCDDLTRL-WMNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----AHHDSVASVFKIKKQNTEKSFDEKSSKCQVTLQNNIEMTTCIFVGRNPEKYI 1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MTWQFVVPAHLRASVSFLNFNLSNCER----KEERVEYYIPGS---TT-----NPEVFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -PADQGSK-----CPESCTQYAREENTQ-IKENIS----DLTCLEIMKA 1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -CMKSSDKKQLPSDKMEQNIKEFNISFQTASGKNTRVSKESLNKSVNIFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNDSHVYAVIEDTMVY-GHLLQDSSGSFLQPEVDTYRPFQGTMGVCPPS 775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEYEIESTKEPTLLSFHTASGKKVKIMQESLDKVKNLFDE
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                      PMID:1899288
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                                                                                  Culver,
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                                           embedded within
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F;56-78/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1> F;79-99/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2> F;100-123/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3> F;124-146/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4> F;147-167/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4> F;147-167/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5> F;168-191/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7> F;192-215/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7> F;216-227/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7> F;216-227/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9> F;216-227/Domain: carboxyl-terminal propeptide #status predicted <CTP> F;426-440/Domain: carboxyl-terminal propeptide #status predicted <CTP> F;425/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-20, 'X', 22-440 <VIS>
A; Residues: 1-20, 'X', 22-440 <VIS>
A; Residues: 1-20, 'X', 22-440 <VIS>
A; Residues: 1-20, 'X', 22-440 <VIS>
A; Residues: 1-20, 'X', 22-440 <VIS>
A; Mikol, D.D.; Stefansson, K.

J. Cell Biol. 106, 1273-1279, 1988
A; Title: A phosphatidylinositol-linked peanut agglutinin-binding glycoprotein A; Reference number: A30187; MUID:88198371; PMID:3283151
A; Accession: A30187
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A; Map position: 17q11.2-17q11.2
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A; Residues: 25-29, 'H', 31, 'H', 33-44, 'D', 46-50, 'P'
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GMVTNTSLTSSTKSSPTPMTLSITSGMPN-----NFSEMPQQSTTLNLWREET
                                                                                                                                                    -----TFAPSFQQEASRQGLTVSFIPY------
                                                                                                                                                                                                                                                                VPAQKLQQHTHEKPCNTSFSYLVA-SAIPSQDLYFGSFCPGGSIKQIQVKQNISVTLR--
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                                                                                                        VTKIPKQYRTKETTFGATLSKDTTFTSTDKAFVPYPEDTSTETINSHEAAAATLTIHLQD
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probable protein kinase PTK2 (EC 2.7.1.-) - y N.Alternate names: probable membrane protein C;Species: Saccharomyces cerevisiae C;Date: 05-May-1995 #sequence\_revision 08-Sep C;Accession: S57078; S71681 R;Huang, M.E.; Chuat, J.C.; Galibert, F. submitted to the Protein Sequence Database, SA;Reference number: S57052

08-sep-1995

#text\_change

24-Sep-1999

September

yeast (Saccharomyces cerevisiae) n YJR059w; protein J1725

RESULT S57078

Qy 617 EIFSLDEDVLE	Db 533 TDATR	Qy 564 WDRGLPSLTSV	Db 487NTE	436 YTP	Db 376 IKFCHDNGIAF	Qy 432 V	Oy 398 Db 321 TFYLLKVPTTTYTT	Qy 342 NKIYVVDLSNE :  : Db 281VYAL	Qy . 285IPGSTTNI ;       Db 223 IRMLPLPIANI	Db 169 SNSMASHHFPN	. 111	Db 53 KRPTSPSISGSGS	Qy 157 DGVTH-SISG-	Qy 100 MSGPCPFGEVC	Query Match Best Local Similarity Matches 172; Conser	A; Residues: 1-818 < MANN A; Cross-references: EMBL: 2. R; Huang, M.E.; Manus, V; & R; Huang, M.E.; Manus, V; & R; Huang, M.E.; Manus, V; & R; Hitle: Analysis of a 62 A; Title: Analysis of a 62 A; Reference number: \$71676 A; Recession: \$71681 A; Status: nucleic acid sequal A; Status: nucleic acid sequal A; Residues: 1-818 < HUAN A;
DVLPKPSFHHHSFWVNISNCSPTSGKQLDLLFSVTLTPRTVDLTVILIAAVGG	::	SLTSVSWNISVPRDQVACLTFFKERSGVVCQTGRAFMIIQEQRTRAE	IQVKQNISVTLRIFAPSFQQEASRQGLTVSFIPVFKEEGVFTVTPDTKSKVYLRTPN	PEVMYFDAKKHYPEKFQKPYNPLAMDSYALGIMLITMINNIIPFIDSC	CHDNGIAHRDLKPENVLISKEGICKLTDEGISDWYHVIPHDYTSPVKTCQGMIGSPP	SWKLL	SFLCDDLTRLWMNVEKTISCTDHRYCQRKSYSLQ  :	NERAMSLTIEPRPVKQSRKFVPGCFVCLESRTCSSNLTLTSGSKHKI : :::	STTNPEVFKLEDKQPGNMAGNFNLSLQGCDQDAQSPGILRLQFQVLVQHPQNES 	DELMTWOF	PSDILGTGTGIASTRORDR - AVLDREKEKERARNKERNTHHAGLPQ	GGNSPSSAGARQRSASLHRRKNNASVGFSNGSVSSHKSSVALQ	VVRIGTFCSNGTVSF	MSGPCPFGEVQLQPSTSLLPTLNRTFIWDVKAHKSIGLELQFSIPRLROIGPGESCP  :	2.6%; Score 112.5; DB 2; Length 818; 19.2%; Pred. No. 5.3; vative 127; Mismatches 317; Indels 281;	18 CMAN  18 CMAN  18 CMAN  18 CMAN  Ces: EMBL:Z49559; NID:g1015728; PIDN:CAA89587.1; PID:g1  Manus, V.; Chuat, J.C.; Gallbert, F.  75, 1996  1s of a 62 kb DNA sequence of chromosome X reveals 36 of a 62 kb DNA sequence of chromosome X reveals 36 of a 62 kb DNA sequence of chromosome X reveals 36 of a 62 kb DNA sequence of chromosome X reveals 36 of a 62 kb DNA sequence of chromosome X reveals 36 of a 62 kb DNA sequence of chromosome X reveals 36 of a 62 kb DNA sequence of chromosome X reveals 36 of a 62 kb DNA sequence of chromosome STR2  2: STK2  2: STK2  10R  10R  10R  10R  10R  10R  10R  10
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Pfam; PF00878; CIMR; 13.
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$EQUENCE FROM N.A., AND SEQUENCE OF 823-830; 859-872; 883-890; 920-925; 960-967; 1235-1244; 1349-1354; 1518-1532; 1624-1656; 1658-1667; 1777-1795 AND 1914-1921.
STRAIN-Meishan; TISSUE-Testis;
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Pfam; PF00094; vwd; 4.
Pfam; PF00629; MAM; 2.
Pfam; PF01826; TIL; 5.
Pfam; PF02345; TILa; 5.
SMART; SM00181; EGF; 1.
SMART; SM00137; MAM; 1.
SMART; SM00214; VWD; 4.
PR0SITE; PS00022; EGF_1,
PR0SITE; PS01186; EGF_2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A sperm membrane protein that binds in a species-specific manner the egg extracellular matrix is homologous to von Willebrand factor.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAPACITATION.
SIMILARITY: CONTAINS 2 MAM DOMAINS.
SIMILARITY: CONTAINS 4.5 VWFD DOMAINS.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: BINDS OF THE EGG. MAY
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                                                                                                                                                                                       SM00137; MAM; 1.
SM00214; VWC; 2.
SM00216; VMD; 4.
PS00022; EGF_1;
PS00186; EGF_2;
PS00740; MAM_1;
PS50060; MAM_2;
                                                                                                                                                                            Glycoprotein;
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TION: BINDS IN A SPECIES-SPECIFIC
MAY BE INVOLVED IN GAMETE
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IPR001007;
IPR001846;
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IPR000998; MAM_domain.
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TILa_Cysrich.
VWF_C.
VWF_D.
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   MAM 1.

MAM 2.

53 X HEPTAPEPTIDE REPEATS (APPROXIMATE)
(MUCIN-LIKE DOMAIN).

VWED 1 (PARTIAL).

VWED 2.

VWED 3.

VWED 4.

VWED 5.
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CYTOPLASMIC (PC
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PER_ANTPE STANDARD; PR
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15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last seque
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Period circadian protein.
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               sequence update)
annotation updat
                                                                                                                                                                                                                                                                                                         -----WLNTSVTIPSGHQQPMQLIFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 117;
Pred. No. 3
                                                            PRT;
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Y SIMILARITY.
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                                                            849
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                                                            A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140;
                                                                                                                                                                                         -YTFSHPNNGDVSSKDTDIP-
                                                                                                                                                                                                                -TVPTEKPTIPTEKSTVPTKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA SEQUENCE).

AA SEQUENCE).

AA SEQUENCE).
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Gaps

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728 331 287

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RA REPDETT S.M., TSAI T., ROCK A.L., SAUMAN I.;

RT "Cloning of a structural and functional homolog of the circadian clock RT gene period from the giant silkmoth Antheraea pernyi.";

RL Neuron 13:167-1176(1994).

CC -1- FUNCTION: INVOLVED IN THE GENERATION OF BIOLOGICAL RHYTHMS. THE CC PLOCALIZATION OF THE TIM-PER COMPLEX. LIGHT INDUCES THE DEGRADATION OF THE TIM-PER COMPLEX. LIGHT INDUCES THE DEGRADATION OF PER. NUCLEAR ACTIVITY OF THE CC LOCALIZATION OF PER. NUCLEAR ACTIVITY OF THE CC HETERODINER COORDINATIVELY REGULATES PER AND TIM TRANSCRIPTION CC NEGATIVE FEEDBACK LOOP. DOES NOT APPEAR TO BIND DNA, SUGGESTING INDIAECT TRANSCRIPTIONAL LOOP. DOES NOT APPEAR TO BIND DNA, SUGGESTING INDIAECT TRANSCRIPTIONAL INTESTION (BY SIMILARITY). EXPRESSION CC INDIAECT TRANSCRIPTIONAL INTESTION OF THE ADDUCT HEADS AND IN CC EXHIBITS PROMINENT CIRCADIAN VARIATION IN ADULT HEADS AND IN CC SUBUNIT: FORMS HETERODINER WITH TIMELESS (TIM); THE COMPLEX THEN CC SUBUNIT: FORMS HETERODINER WITH TIMELESS (TIM); THE COMPLEX THEN CC SUBUNITARITY. NUCLEUS (BY SIMILARITY).

CC INTERACTION WITH TIM IS REQUIRED FOR NUCLEAR LOCALIZATION (BY SIMILARITY).

CC INTERACTION WITH TIM IS REQUIRED FOR NUCLEAR LOCALIZATION DOMAINS.

CC INTERACTION WITH TIME STANDARD C-TERMINAL (PAC) DOMAINS.

CC INTERACTION WITH TIME STANDARD C-TERMINAL (PAC) DOMAINS.

CC INTERACTION WITH TIME STANDARD C-TERMINAL (PAC) DOMAINS.

CC INTERACTION WITH TIME STANDARD C-TERMINAL (PAC) DOMAINS.
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Best Local
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Antheraea pernyi (Chinese oak silk moth).
Antheraea pernyi (Chinese oak silk moth).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
Ditrysia; Bombycoidea; Saturniidae; Saturniinae; Saturniini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART;
                                                                                                                                                                                                                                                                                                                                      DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Head, and Thorax;
                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biological
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                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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InterPro; IPR000014; PAS_domain.
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179 VLYATASLISTLGFPKDMWVGRSFIDFVHPRDRNIFASQIINELAIPKIVSLIEETDQIM
                                          193
                                                                              133
                                                                                                                                                           81
                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                             85 PENHFVIEIQKNIDCMSGPCPFGEVQLQPSTSLLPTLNRTFIWDVKAHKSIGLELQFSIP 144
                                      KM-----ALHLP-----WFHPRNVSGFS--IANRSSIKRLCII----ESVF
                                                                              DTNNDKEEAIVYNTSLINPGTACPFG-----
                                                                                                                                                         PDTQIEVECRPEEDVINIPSEEGGA---ADDVLVPSPKQTLQTDNDI-----ADIEVAIP
                                                                                                                                                                                                                                     al Similarity
167; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SM00086; PAC; 1.
SM00091; PAS; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    rhythms;
                                                                                                                                                                                                                                                                                                                  849 AA;
                                                                                                                                                                                                                                       Conservative
                                                                                                                ---IGPGESCPDGVTHSISGRIDATVVRIGTFCSNGTVSRIKMQEGV 192
                                                                                                                                                                                                                                                                                                                                    74
225
370
418
58
74
                                                                                                                                                                                                                                                         2.6%;
18.6%;
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                                                                                                                                                                                                                                                                                                                  94799 MW;
                                                                                                                                                                                                                                     110;
                                                                                                                                                                                                                                                         Pred. No.
                                                                                                                                                                                                                                                                         Score 115.5;
                                                                                                                                                                                                                                                                                                            NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

PAS 1.

PAS 2.

PAC 2.

PAC PAC POLY-SER.

POLY-LYS.

07C8654EEC058770 CRC64;
                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; Phosphorylation
                                                                              ----RPALSNCNGFSCVISMHDGV
                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                     311; Indels 311;
                                                                                                                                                                                                                                                                         Length 849;
                                                                                                                                                                                                                                   Gaps
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J. Virol. 52:177-182(1984)I- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.	SPR
reticuloendotheliosis virus strain T and its cellular homolog, the	
15009850; PubMed=6090694; en K.C., Eggleton K., Temin H.M.;	
SEQUENCE FROM N.A. STRAIN-A:	
Avian reticuloendothei10515 vitus. Viruses; Retroid viruses; Retroviridae; Gammaretrovirus. NCBI_TaxID=11636;	
GP22].	
21-JUL-1900 (Rel. 01, Cleaced) 21-JUL-1986 (Rel. 01, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) ENV polyprotein (Coat polyprotein) [Contains: Coat protein GP73; Coat	
T 4 VIRE STANDARD; ENV_AVIRE STANDARD;	RESUL ENV_A ID AC
PNYHRNNMNNNQFQQPLGN	Вb
779 ICSRAPTAKLATEEPPPRSPPESESEPYTFSHPNNGDVSSKDTDIPLLNTQEP 831	Qy
713 SRQFRRKQTTCSGGFAQPPSATNPVSTSSQWSSSPVNNVNPFILGVRMQPPMPILSPLPV 772	Db
740 TMVYGHLLQDSSGSFLQPPT 778	Qy
675 TISAANNTPSV-YEKPHN-LKRSSKQMESEPIANKHHCPS 712	Db
LGLIICCVKKKKKKTNKGPAVGIYNGNINTEMPRQPK	Qy
634 KELMKIHREHRCYSKGDRVKVSNEARQKKKE	В
624 DVLPKPSFHHHSFWVNISNCSPTSGKQLDLLESVTLTPRTVDLTVILIAAVGGGVL 679	Qy
586 SGDVIDLTGPGETSGVIVENKSPTMGLKTGKPIRLTESSLTKHNÄEME 633	Db
575 SWNISVPRDQVACLTEFKERSGVVCQTGRAFMIIQEQRTRAEEIFSLDE 623	Qy
542 QRYFNSHQSNAFVDNNLLPSRNPLYLSAPHFSESIKNVPSAMEY 585	Db
SRQGLTVSF1PYFKEEGVFTVTPDTKSKVYLRTPNWDRG	Qy
508 SVILGGISPHHEYDSKSSTETPLSY	망
458 SLVLVPAQKLQQHTHEKPCNTSFSYLVASAIPSQDLYFGSFCPGGSIKQIQVKQNISVTL 517	Qy
457 TKPAEIAKQQMSKRCQDLAHFMEMLIEEQPKPVDDLRLEIQDADHSYYERD 507	DЪ
TISCTDHRYCORKSYSLOVPSDILHLPV	Qy
397 FINPWSKKLEFYTGKHYIIEGPANPDVFQNPENVLKLTEEQKNQAKMYRDSIIRIMKDVL 456	Db
FVPGCFVCLESRTCSSNLTLTSGSK	Qy
355 DLGYLQEIYGSLVKEGNVTRSKTYRMMTQNGHYMKVETEWSA 396	Dβ
MAGNFNLSLQGCDQDAQSI	VΩ
299 SAFKTSNEVLAKTVSFVIRHSADGNLEYIDAESVPYLGYLPQDITNRDALLLYHPG 354	DЪ
259HLRASVSFLNFNLSNCERKEERVEYYIPGSTTNPEVFKLEDKQPG 303	Qγ
:     :	Db
228 EGEGSATIMSANYPEGFP258	Qy

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RESULT
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01-FEB-1995 (
15-JUL-1998 (
Hypothetical
YHR155W.
                                                                                                                                  YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002050; Env_poly Pfam; PF00429; ENV_polyproteif Coat protein; Glycoprotein; T CHAIN 1 391
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EMBL; X01455; CAA25686.1; -.
PIR; A03999; VCVDAR.
HSSP; P03385; 1MOF.
                                                                                                     YHV5_YEAST
P38851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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 Eukaryota;
               Saccharomyces cerevisiae (Baker's yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             318
                                                                                                                                                                                             533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          314 QGCDQDAQSPGILRLQFQVL-VQHPQNESNKIYVVDL-----SNERAMSLTIEPRPVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              366 QSRKFVPGCFVCLESRTCSSNLTLTSGSKHKIS---FLC---DDLTRLWMNVEKTISCTD
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                                                                                                                                                                                                                                                       KIRKLQEDLLARKRALYDNPLWNGLNGFLPYLLPSLGPLF-
                                                                                                                                                                                                                                                                                EIFSLDEDVLP-KPSFHHHSFWVNISNCSPTSGKQLDLLFSVTLTPRTVDLTVILIAAVG
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                                                                                                                                                                                            -GLILFLTLG----PCIRKTLTRIIHDKIQGSKNPRISPAVQATPNR
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89; Conserv
Fungi; Ascomycota;
                                          (Rel. 31, Created)
(Rel. 31, Last sequence update)
(Rel. 36, Last annotation update)
1 143.6 kDa protein in SPO16-REC104
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                                                                                                                     STANDARD;
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
CD2560ADFC026D32 CRC64;
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Pred. No. 0.
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Saccharomycotina;
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                                                                                                                                                                                                                                                                                                                                                                                                    . 64;
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                                            intergenic
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 Saccharomycetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 170;
                                                                                                                                                                                             57.
                                            region
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Best Local S
Matches 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 265:2077-2082(1994).
-!- SIMILARITY: STRONG, TO YEAST SIP3
-!- SIMILARITY: CONTAINS 1 PH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.
Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser
Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K
Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
Vaudin M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U10397; AAB68977.1; -. PIR; S46754; S46754.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=S288c / AB972;
MEDLINE=94378003; PubMed=8091229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00233; PH; 1.
PROSITE; PS50003; PH_DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00169; PH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
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YDKSPKHVSSRMLHMQRG----DGLRFNMSVFFTDRRAVASKLQFLIENKAMHIPKGEKE
                                                               LQVPKEL-VLLRYSSVWCPNNKQKFASMAFVTLNHIYVYLNISGFSYLRRIDLLDIDSIE
                                                                                           IQVKQNISVTLR---TFAPSFQQE-ASRQGLTVSFIPYFKEEGVFTVTP----
                                                                                                                              NDLSYLVNPLKGSSVH----KPATVSNSSRFSVSYPDYYPYSLKVDDIQFRSIFFSVNHDF
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"cloning, chromosomal mapping and
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                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-97384941; PubMed-9242436;
MCAllister K.A., Haugen-Strano A., Hagevik S., Brownlee H.A.,
Collins N.K., Futreal P.A., Bennett L.M., Wiseman R.W.;
"Characterization of the rand mouse homologues of the BRCA2 breast cancer susceptibility gene.";
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Sharan S.K., Bradley A.;
"Murine Brca2: sequence, mu
Genomics 40:234-241(1997).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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  SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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Res. 57:3121-3125(1997).
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Mikol D.D., Gulcher J., Stefansson K.;
"The oligodendrocyte-myelin glycoprotein belongs to
of proteins and contains the HNK-1 carbohydrate.";
J. Cell Biol. 110:471-479(1990).
                                                                                                                                                                                                                                                                                                                                                                                                            :01-NOV-1991 (Rel. 20, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
01igodendrocyte-myelin glycoprotein precurs
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"The gene encoding the oligodendrocyte-myelin glycoprotein embedded within the neurofibromatosis type 1 gene.";
Mol. Cell. Biol. 11:906-912(1991).
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Mammalia; Eutheria;
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Pfam; PF01462; LRRUT; 1.
PRINTS; PR00019; LEURICHRPT
SMART; SM00370; 1.PB.
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SMART; SM00369; LRR_TYP;
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Mikol D.D., Stefansson K.;

"A phosphatidylinositol-linked peanut agglutinin-binding glycoprote in central nervous system myelin and on oligodendrocytes.";

J. Cell Biol. 106:1273-1279(1988).

-I- FUNCTION: CELL ADHESION MOLECULE CONTRIBUTING TO THE INTERACTIV PROCESS REQUIRED FOR MYELINATION IN THE CENTRAL NERVOUS SYSTEM.

-I- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.

-I- TISSUE SPECIFICITY: OLIGODENDROCYTES AND MYELIN OF THE CENTRAL NERVOUS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structure and chromosomal localization oligodendrocyte-myelin glycoprotein."; J. Cell Biol. 111:2673-2679(1990).
                                                                                    s SWISS-PROT entry is copyright. It is produced through a ween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                    PTM: O-GLYCOSYLATED IN ITS SER/THR-RICH REPEAT DOMAIN (POTENTIAL) SIMILARITY: CONTAINS 8 LEUCINE-RICH REPEATS (LRR). CAUTION: DO NOT CONFUSE OLIGODENDROCYTE-MYELIN GLYCOPROTEIN (OMG) WITH MYELIN-OLIGODENDROCYTE GLYCOPROTEIN (MOG).
                                                          rmatics Institute. There are no restinstitutions as long as its content
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STRAIN-S288C;
MEDLINE-96437976; PubMed-8840504;
MEDLINE-96437976; PubMed-8840504;
                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyces: Saccharomyces
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                                                       "Analysis
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Igarashi K.;
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                         M.-E., Manus V., Chuat J.-C., Galibert F.;
ysis of a 62 kb DNA sequence of chromosome
ng frames and a gene cluster with a counter
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ura K., Michael
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00107;
PROSITE; PS00108;
PROSITE; PS50011;
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InterPro; IPR002290; Sei
Pfam; PF00069; pkinase;
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CHARACTERIZATION.
MEDLINE=97299648; PubMed=9154797;
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                                                                                                                  NKIYVVDLSNERAMSLTIEPRPVKQSRKFVPGCFVCLESRTCSSNLTLTSGSKHKI----
                                                                                                                                             IRMLPLPIANPNDFLPEDMKQYSVHLTDNFVFDTDNKPIGSGGSSEVR-KVKSSYRQKD-
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PS00118; PROTEIN_KINASE_DOM; 1.
PS50011; PROTEIN_KINASE_DOM; 1.
Se; Serine/threonine-protein kinase; ATP-binding
255 562 PROTEIN KINASE
261 269 ATP (BY SIMILARITY).
388 388 BY SIMILARITY.
388 388 BY SIMILARITY.
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Pred. No. 1.
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                                                      Query Match
Best Local S
Matches 185
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Q92545;
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bidinformatics and the EMBL outstation the European Bidinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                      Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayasi Y., Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.; "Prediction of the coding sequences of unidentified human genes. The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced analysis of cDNA clones from cell line KG-1 and brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Mammalla; Eutherla; Primates; NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RW1 protein (Fragment)
RW1 OR KIAA0257
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence u)
15-JUN-2002 (Rel. 41, Last annotation
                                                                                                                                              EMBL; D87446; BAA13387.1; -. NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                        DNA Res. 3:321-329(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97191544; PubMed-9039502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Bone marrow;
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                                                                        Score 112.5;
Pred. No. 5.2;
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SN_MOUSE STANDARD; PRT; 1694 AA.

2 Q62230; O55216; Q62228; Q62229;

30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15 Slaloadhesin precursor (Sialic acid binding Ig
1) (Sheep erythrocyte receptor) (SER).

SN OR SA.
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MEDLINE-98325385; Pubb
May A.P., Robinson R.C
"Crystal structure of
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[3]
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"Staloadhesin, a macrophage stallc acid binding receptor for haemopoletic cells with 17 immunoglobulin-like domains.";
EMBO J. 13:4490-4503(1994).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-C57BL/6; T: MEDLINE-91266893;
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MEDLINE-95009950;
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10:1661-1669(1991).
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98325385; PubMed=9660955;
, Robinson R.C., Vinson M., Crocker P.R., Jones E.Y. structure of the N-terminal domain of sialoadhesin with 3' sialyllactose at 1.85 A resolution.";
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TO76997;

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T 30-MAY-2000 (Rel. 39, Created)

T 30-MAY-2000 (Rel. 39, Last sequence update)

T 15-JUN-2002 (Rel. 41, Last annotation update)

E Putative neurotrophin receptor LTRK 1 precursor (EC Lymnaea stagnalis (Great pond snail).

Stymnaea stagnalis (Great fond snail)
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SEQUENCE
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Vreugdenhil E., Smit A.B., Ibanez C.F., Geraerts
                                                                                                                                                                                                                                                                           Bulloch A.G.M.;
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Best Local
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MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00219; TYTRC; 1.

PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.

PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.

PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00013; LRRNT;
SMART; SM00369; LRR_TY
SMART; SM00219; TyrKC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U61728; AAC26840.1; -. HSSP; P08631; 1AD5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                       ACT_SITE
                                                                                                                                                                                                                                                                                                                                                BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD000001; Euk_pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00109; TYRKINASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
 158
                    341
                                                                                                                                                        203
                                                                 305
                                                                                                             261
                                            99
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                                                                                                                                  4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: CONTAINS 2 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                       PRNVSGFSIANRSSIKRLCIIESVFEGEGSATLMSANYPEGFPEDELMTWQFVVPAHL--
                   SNKIYVVDLSNERAMSLTIEPRPVKQSRKFVPGCFVCLESRT----CSSN------LTLT
----VIKLELRGQSKLT----
                                                                                       QDGVTTERVDRSKNHRNTTASSGAHRVTSGEPLGDRV---TTRSTTAP----
                                                                                                                                   PRRFRLWTRANVLTV -- ISILTSILSGAGCSPLSQ -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                              .ne-rich
                                           ASRNTTMAGTKCSLQVDLSTFACPADCQCNATSEGMVVSCVTPDTLR-EFPVIAREVARA
                                                                                                                                                                              119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SM00369; LRR_TYP;
SM00219; TYTKC; 1
                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR002011;
IPR001245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR001611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR003591;
IPR002011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR00037
                                                                MAG----NFNLSLQGCDQDAQ-----
                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat;
                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pkinase; 1.
LRR; 1.
                                                                                                                                                                                                                                               789
89054 MW;
                                                                                                                                                                                       2.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRR_typ.
RTKinaseII.
                                                                                                            -RASVSFLNFNLSNCERKEERVEYYIPGSTTNPEVFKLEDKQPGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tyr_pkinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRR_Nterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat;
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 SLKTELKF----FTCLKHLTIENCGLNNIQGIAFKTLT
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N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
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PHOSPHORVLATION (AUTO-)
PHOSPHORYLATION (AUTO-)
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Pred. No. 2
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N-LINKED
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(BY SIMILARITY)
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ON (AUTO-) (BY SIMILARITY).

ON (AUTO-) (BY SIMILARITY).
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                                                                                                                                   -LPSDN-----
                                                                -SPGILRLQFQVLVQHPQNE
                                                                                                                                                                                                 Length
                                                                                                                                                                                                                         CRC64;
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(POTENTIAL).
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                                                                                                                                   --PAHVGV
                                                                                                                                                                              212;
                                                                                       -DQVPGD
                                                                                                                                                                                                                                                                                                                                                                                                                                          LTRK
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                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Complement-activating component of Ra-reactive factor precursor
(EC 3.4.21.) (Ra-reactive factor serine protease p100) (RaKF)
(Mannan-binding lectin serine protease 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOUSE
                                                    +++
                                                                                                                                                                                                                                                                                                                                     Blochem Biophys. Res. Commun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-93176166; pubMed-8439319;
Takahashi A., Takayama Y., Hatsus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BALB/c; TISSUE-Liver; MEDLINE-94179811; PubMed-813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P98064;
01-FEB-1996
                                                                                                                                                                                                                <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 465-704 FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takayama Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.,
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                                                                                                                                                                                                                                                                                                                                                                                          serum
                                                                                                                                                                                                                                                                                                                                                                                                                                    Takahashi A., Takayama Y., Hatsuse H., Presence of a serine protease in the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MASP1
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                                                                                                                                                                                                                                                                                                                                                                                                                    the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     kayama Y., Takada F., Takahashi A., Ka100-kDa protein in the C4-activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immuno1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tor is a a and Cls.
LINKED BY A DISULFIDE BOND.

TISSUE SPECIFICITY: LIVER.

DOMAIN: CRARF HAS A MODULE ORGANIZATION SIMILAR SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.

SIMILARITY: CONTAINS 2 CUB DOMAINS.
                                                                                                                                                 Chem. Blophys. Res. Commun. 190:681-687(1993).

FUNCTION: COMPONENT OF THE BACTERICIDAL RA-RACTIVE FACTOR RARF WHICH SPECIFICALLY BINDS TO RA AND R2 POLYSACCHARIDES EXPRESSED I CERTAIN ENTEROBACTERIA. IT TRIGGERS THE ACTIVATION OF COMPLEMENT CASCADE BY ACTIVATING THE C4 AND C2 COMPONENTS. IT ACTIVATES THE C4 COMPONENT BY CLEAVING THE ALPHA-CHAIN OF C4.

SUBUNIT: RARF CONSISTS OF A COMPLEMENT-ACTIVATING COMPONENT (CRARF) AND A POLYSACCHARIDE-BINDING (MANNOSE-BINDING) COMPONENT. CRARF IS AN HETERODIMER OF A HEAVY (P70) AND A LIGH CHAIN (29)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TP--DTKSKVYLRTPNWDRGLPSLTSVSWNISVPRDQVACLTFFKERSGVVCQTGRAFMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OR CRARF
                                                                                                                                                                                                                                                                                                                                                                                                               nce of a serine protease in the complement-activating complement-dependent bactericidal factor, RaRF, in mo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKGQANQTFHLYDQTTPASSIH----IPLSNIPPR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152:2308-2316(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             new serine protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed-8133044;
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Query Match
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PROSITE; PSO1180; CUB; 2.

PROSITE; PSO1186; EGF_2; 1.

PROSITE; PSO1187; EGF_CA; 1.

PROSITE; PSO1187; EGF_CA; 1.

PROSITE; PSO0134; TRYPSIN_HIS; 1.

PROSITE; PSO0134; TRYPSIN_HIS; 1.

PROSITE; PSO0135; TRYPSIN_Scr; 1.

Hydrolase; Complement pathway; Serine; Glycoprotein; Sushi; Repeat; Signal; EC
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Interpro; IPRO00859;
Interpro; IPRO01314;
Interpro; IPRO01561; E
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SEQUENCE FACE.

STRAIN-20016719; PubMed=11130712;

MEDLINE-21016719; PubMed=11130712;

Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Buehler E., Chan A., Chao O., Chen H., Cheuk R.F., Chin C.W.,

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Chang M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Fujii C.Y.,

Chung P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fughes B., Huizar L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative receptor protein kinase TMK1 precursor (EC 2.7.1.-).
TMK1 OR ATIG66150 OR F15E12.4.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                       Meyerowitz E.M., Bleecker A.B., "The TMKI gene from Arabidopsis codes and biochemical characteristics of a r Plant Cell 4:1263-1271(1992).
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MEDLINE-93076110; PubMed-1332795;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----IPYFKEEGVETVTPDTKSKVYLRTPNWDRG-----LPSLTSVSWNISVPRDQVA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FCGEKSPEPISTQTHSVQILFRS-----DNSGENRGWRLSYRAAGNECPKLQPPVYGKIE
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8; Mismatches
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SMART; SM00221; STYKC; 1.
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Transferase; Serine/threonine-protein kinase;
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TISSUE SPECIFICITY: FOUND IN MOST TISSUES.
PTM: AUTOPHOSPHORYLATED ON SERINE AND THREONINE RESIDUES.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
SIMILARITY: CONTAINS 9 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: PROBABLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00560;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s requires a license agreement (San email to license@isb-sib.ch).
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; IPRO03592;
; IPRO03591;
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IPR002290;
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                                                         repeat;
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                                                         STY_pkinase.
Ser_thr_pkinase.
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                                                                                                                                                                                                                                                                                                                  POTENTIAL.

PUTATIVE RECEPTOR PROTEIN KINASE TMK1.

EXTRACELULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

LRR 1.

LRR 2.

LRR 3.

LRR 4.

LRR 5.

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RESULT 14
DPB2_YEAST
ID DPB2_YE
AC P24482
DT 01-MAR
DT 01-MAR
DT 01-NOV
DT 15-JUN
DE DNA PO
DE SUBUBL
GN DPB2 O
OS Saccha
OC EUKBIY
OC SACCHA
OC EUKBIT
RN [1]
RN [1]
RP SEQUEN
RC STRAIN
RA ATAK1
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Best Local S
Matches 128
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SEQUENCE
                                                                            Saccharomyces cerevisiae (Baker's yeast
Eukaryota; Fungi; Ascomycota; Saccharon
Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                      DPB2_YEAST STANDARD;
P24482; Q06622;
O1-MAR-1992 (Rel. 21, Created)
O1-NOV-1997 (Rel. 35, Last seq
15-JUN-2002 (Rel. 41, Last ann
 MEDLINE-91271241;
Araki H., Hamatak
                                                                                                                  DPB2 OR YPR175W OR P9705.
                                        SEQUENCE FROM N.A.
                                                                NCBI_TaxID=4932;
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                                                                                                                                          polymerase epsilon
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                                                                                                                                                                                                                                                                                                                                                                             MIPQ-----ELTTLPNLKTLDVSSNKLFGKVPGF----
                                                                                                                                                                                                                                                                                                                                                                                                     FIPYFKEEGVFTVTPDTK-----SKVYLRTPNWDRGLPSLTSVSWNISVPRDQVACLTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FKSSVSVDLDKDSNSFCLSSPGECDPRVKSLLLIASSFDYPPRLAESWKGNDPCTN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NESNKIYVVDLSNERAMSLTIEPRPVKQSRKFVPGCFVCLESRTCSSNLTLTSGSKHKIS
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  PubMed=2052544;
e R.K., Johnston
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Last annotation updat
n subunit B (EC 2.7.7.
                                                                            (Baker's yeast).
cota; Saccharomycotina; Sacclaromycetaceae; Saccharomyces
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Pred. No. 2.8;
82; Mismatches
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The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=S288c / AB972;
MEDLINE=97313271; Pub
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                                                                                                                                                            91
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Local Similarity 17.8%;
hes 123; Conservative 1
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MISCELLANEOUS: IN EUKARYOTES THERE ARE FIVE DNA POLYMERASES:
ALPHA, BETA, GAMMA, DELTA, AND EPSILON WHICH ARE RESPONSIBLE
DIFFERENT REACTIONS OF DNA SYNTHESIS
SIMILARITY: TO OTHER SPECIES DNA POLYMERASE EPSILON, SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT:
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CATALYTIC ACTIVITY: N deoxynucleoside triphosphate =
; M61710; AAA34576.1;
; U25842; AAB68109.1;
A39698; A39698.
S0006379; DPB2.
                                                                                                                                                                                                     VSRIKMQEGVKMALHLPWFHPRNVSG------FSIANRSSIKRLCI-----
                                                                                                                                                            IQEMKEREKVEWSHEHPIQHEENILGRIDDDENNSDDEMPIAADSSLQNVSLSSPMRQPT
                                                                  ERDEYKQPFKPESSKALDWRDYFKVINASQQQRFSYNPHKMQFIFVPNKKQNGLGGIAGF
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461 461 F

524 524 568 1

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                                                                                                                                                                                                                                                 Score 109.5; I
Pred. No. 2.1;
06; Mismatches
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K -> R (IN REF. 1).
V -> F (IN REF. 1).
E -> Q (IN REF. 1).
T -> I (IN REF. 1).
5C01647BD2B6A39A C
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     This SWISS-PROT entry is copyright. It is produced through a cetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                 "Microtubule-associated protein MAP2 motif with tau protein."; Science 242:936-939(1988).
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[2]
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MEDLINE-89083571; PubMed-3205744;
Wang D., Lewis S.A., Cowan N.J.;
"Complete sequence of a cDNA enco
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MEDLINE-89043973; Pubmed-3142041;
Lewis S.A., Wang D., Cowan N.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
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                                                                                                        FUNCTION: THE EXACT FUNCTION OF MAP2 IS UNKNOWN BUT STABILIZE THE MICROTUBULES AGAINST DEPOLYMERIZATION. SEEM TO HAVE A STIFFENING EFFECT ON MICROTUBULES. SIMILARITY: CONTAINS 3 TAU/MAP REPEATS.
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Best Local
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PIR; S06467; S06467.
PIR; A40115; A40115.
MGD; MGI:97175; Mtap2.
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TFSHPNNGDV-----
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                                                                      SYESSGEHESLIMESLKPDEGKKETSPET--SLIQDEVALKLSVEIPCP--PPVSEAD--
                                                                                                                                                                    LKFEVAQELTLSSEAPQEADSFMGVESGHIKEGGKVNETEVKEKVTKPDLVHQEAVDKEE
                                                                                                                                                                                                                  I----YNGNINTEMPROPKKF
                                                                                                                                                                                                                                                                  TKADQGLDFAATKAEPSQLDIKVSDFGQMASGM-----
                                                                                                                                                                                                                                                                                                                                                                  DSKEHAKESEEMGGKVELFGLGITYDQASTKELITTKDTSPEKTEKGLSSVPEVAEVEPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAVEKMPCFPIESKEEEDKAEQAK-----VTGGQTIQVETSSESPFPAKEYYKNGTVMA
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                                                                                                                                                                                                                                                                                                                SGKQLDLLFSVT-LTPRTVDLTVILIAAVGGGVLLLSALGLIICCVKKKKKKTNKGPAVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSLIEVKLAAAGRVKDEFTAEKEATPPTSADKSGLSREFDHDRKANDKLDTVLEKSEEHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDTKSKVYLRTPNWDRG------LPSLTSVSWNIS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LDTISPKNQHDEKELQAKASQPSPPAQEAGYSTLA---QSYTPG----HPSELPEEPSSP
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                                                                                                                       DSSGSFLQPEVDTYRPFQGTMGVCPPSPPTICSRAPTAKLATEEPPPRSPPESESEPY
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ules; Repeat; Calmodulin-binding
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-SSKDTDIPLL--NTQEPM-----EPAE
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TAU/MAP MOTIF.
TAU/MAP MOTIF.
MW; 200BC59E36053BCA C
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Db 1190 -LSTDEKGEVQMEFIQLPKEESTETPDIPAIPSDVTQPQPEAIVSEPAE 1237

Search completed: November 11, 2002, 11:31:35 Job time : 35 secs